

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 21.0896 Seconds  
(without alignments)  
120.578 Million cell updates/sec

Title: US-09-641-802-31  
Perfect score: 48  
Sequence: 1 VESYVPLFP 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	48	100.0	9	2	AAW42101	Aaw42101 Colostrin
2	48	100.0	9	4	AAB72529	Aab72529 Colostrin
3	48	100.0	9	4	AAB72276	Aab72276 Colostrin
4	48	100.0	9	4	AAB72561	Aab72561 Colostrin
5	48	100.0	9	5	AAO14607	Aao14607 Neural ce
6	48	100.0	9	5	AAM51067	Aam51067 Colostrin
7	48	100.0	9	5	AAE20258	Aae20258 Colostrin
8	44	91.7	8	4	AAE07189	Aae07189 Colostrin
9	44	91.7	9	4	AAE07199	Aae07199 Modified

10	34	70.8	12	7	ADE12722	Ade12722	Hev b	III
11	34	70.8	12	7	ADE12457	Ade12457	Hev b	III
12	33	68.8	9	6	ABR02117	Abr02117	Human	can
13	33	68.8	10	6	ABR02228	Abr02228	Human	can
14	33	68.8	10	6	ABR02236	Abr02236	Human	can
15	33	68.8	10	6	ABR01994	Abr01994	Human	can
16	33	68.8	10	6	ABR02606	Abr02606	Human	can
17	33	68.8	10	6	ABR03056	Abr03056	Human	can
18	33	68.8	10	6	ABR02424	Abr02424	Human	can
19	33	68.8	15	5	ABP46299	Abp46299	Human	BLy
20	33	68.8	15	6	ABR30067	Abr30067	Human	can
21	33	68.8	15	6	ABR30111	Abr30111	Human	can
22	33	68.8	15	6	ABR29962	Abr29962	Human	can
23	33	68.8	15	6	ABR30102	Abr30102	Human	can
24	33	68.8	15	6	ABR30015	Abr30015	Human	can
25	33	68.8	15	6	ABR30048	Abr30048	Human	can
26	33	68.8	15	6	ABR29971	Abr29971	Human	can
27	33	68.8	15	6	ABR30004	Abr30004	Human	can
28	33	68.8	16	5	ABP46252	Abp46252	Human	BLy
29	29	60.4	9	6	ABR02132	Abr02132	Human	can
30	29	60.4	9	6	ABR02528	Abr02528	Human	can
31	29	60.4	9	6	ABR02946	Abr02946	Human	can
32	29	60.4	9	6	ABR02332	Abr02332	Human	can
33	29	60.4	10	5	AAU82797	Aau82797	Human	Cal
34	29	60.4	10	6	ABR02235	Abr02235	Human	can
35	29	60.4	10	6	ABR02609	Abr02609	Human	can
36	29	60.4	10	6	ABR02053	Abr02053	Human	can
37	29	60.4	10	6	ABR02387	Abr02387	Human	can
38	29	60.4	13	2	AAW05005	Aaw05005	Peptide	r
39	29	60.4	13	2	AAW41667	Aaw41667	Immunomod	
40	29	60.4	13	4	AAU17675	Aau17675	Novel	sig
41	29	60.4	13	6	ABO27231	Abo27231	Gab3	PXXP
42	29	60.4	13	7	ADB94383	Adb94383	Novel	hum
43	29	60.4	14	1	AAP80629	Aap80629	Synthetic	
44	29	60.4	14	2	AAW05004	Aaw05004	Peptide	r
45	29	60.4	14	2	AAW41666	Aaw41666	Immunomod	
46	29	60.4	14	5	ABP46646	Abp46646	Human	BLy
47	28	58.3	10	5	AAU82854	Aau82854	Human	Cal
48	28	58.3	17	2	AAW39045	Aaw39045	Peptide	r
49	27	56.2	11	5	AAE18839	Aae18839	Human	cal
50	27	56.2	12	6	ABR58779	Abr58779	Alzheimer	
51	27	56.2	17	5	ABG62499	Abg62499	Eubacteri	
52	26	54.2	9	6	ABR02683	Abr02683	Human	can
53	26	54.2	9	6	ABR01867	Abr01867	Human	can
54	26	54.2	9	6	ABR02933	Abr02933	Human	can
55	26	54.2	9	6	ABR02140	Abr02140	Human	can
56	26	54.2	9	6	ABR02483	Abr02483	Human	can
57	26	54.2	9	6	ABR02279	Abr02279	Human	can
58	26	54.2	9	6	ABR03110	Abr03110	Human	can
59	26	54.2	10	6	ABR03215	Abr03215	Human	can
60	26	54.2	10	6	ABR02390	Abr02390	Human	can
61	26	54.2	10	6	ABR02264	Abr02264	Human	can
62	26	54.2	10	6	ABR02798	Abr02798	Human	can
63	26	54.2	10	6	ABR02001	Abr02001	Human	can
64	26	54.2	10	6	ABR02622	Abr02622	Human	can
65	26	54.2	11	2	AAAY27116	Aay27116	EE	antige
66	26	54.2	11	4	AAE11116	Aae11116	Tryptic	p

67	26	54.2	13	5	AAE24109	Aae24109	Rice C039
68	26	54.2	14	5	ABP46522	Abp46522	Human BLy
69	26	54.2	14	5	ABP46699	Abp46699	Human BLy
70	26	54.2	15	4	AAB97743	Aab97743	gp100 der
71	26	54.2	15	4	AAB97741	Aab97741	gp100 der
72	26	54.2	15	4	AAB97742	Aab97742	gp100 der
73	26	54.2	15	4	AAB98132	Aab98132	Interfero
74	26	54.2	15	4	AAB98131	Aab98131	Interfero
75	26	54.2	15	4	AAB98133	Aab98133	Interfero
76	26	54.2	15	6	ABR30033	Abr30033	Human can
77	26	54.2	15	7	ADC99931	Adc99931	Murine Sa
78	26	54.2	15	7	ADD24103	Add24103	Breast ca
79	26	54.2	16	5	ABP46250	Abp46250	Human BLy
80	26	54.2	18	5	AAO14472	Aao14472	Peptide f
81	26	54.2	18	6	ABU08859	Abu08859	Loblolly
82	25	52.1	7	2	AAV17016	Aay17016	Heat shoc
83	25	52.1	7	4	AAU72158	Aau72158	Melanoma
84	25	52.1	7	5	AAU80708	Aau80708	Javelin p
85	25	52.1	8	2	AAV16845	Aay16845	Heat shoc
86	25	52.1	10	2	AAV45435	Aay45435	Immunogen
87	25	52.1	10	6	ABR06228	Abr06228	Human can
88	25	52.1	11	2	AAR86908	Aar86908	Tyrosine
89	25	52.1	14	7	ADC98012	Adc98012	Signallin
90	25	52.1	15	2	AAW42254	Aaw42254	Biotinyla
91	25	52.1	15	2	AAW42265	Aaw42265	Biotinyla
92	25	52.1	15	4	AAG80099	Aag80099	Chemokine
93	25	52.1	15	5	ABG92731	Abg92731	A. nidula
94	25	52.1	15	5	ABG92730	Abg92730	A. nidula
95	25	52.1	15	6	ABR32153	Abr32153	Human can
96	25	52.1	15	6	ABR31871	Abr31871	Human can
97	25	52.1	15	6	ABR31736	Abr31736	Human can
98	25	52.1	15	6	ABR31737	Abr31737	Human can
99	25	52.1	15	6	ABR31709	Abr31709	Human can
100	25	52.1	15	6	ABR32272	Abr32272	Human can

# ALIGNMENTS

## RESULT 1

AAW42101

ID AAW42101 standard; peptide; 9 AA.

XX

AC AAW42101;

XX

DT 09-SEP-1998 (first entry)

XX

DE Colostrinin derived nanopeptide.

XX

KW Colostrinin; nanopeptide; NP; central nervous system; CNS;

KW neurological disorder; mental disorder; dementia; Alzheimer's disease;

KW motor neurone disease; Parkinson's disease; psychosis; neurosis;

KW immunological deficiency; cancer therapy; stimulantion; modulator;

KW dietary supplement; cachexia; inhibition.

XX

OS Homo sapiens.

XX

PN WO9814473-A1.  
 XX  
 PD 09-APR-1998.  
 XX  
 PF 03-OCT-1997; 97WO-GB002721.  
 XX  
 PR 03-OCT-1996; 96PL-00316416.  
 XX  
 PA (HIRS-) HIRSZFELD INST IMMUNOLOGY & EXPERIMENTAL.  
 PA (GEOR-) GEORGIADIS BIOTECH LTD.  
 XX  
 PI Janusz M, Lisowski J, Dubowska-Inglot A;  
 XX  
 DR WPI; 1998-250967/22.  
 XX  
 PT Use of colostrinin, or derived nonapeptide for treating chronic diseases  
 PT of the central nervous system - and immune system, also as dietary  
 PT supplement and for inhibiting development of Alzheimer's disease.  
 XX  
 PS Claim 51; Page 27; 34pp; English.  
 XX  
 CC This is the amino acid sequence of the colostrinin derived nanopeptide  
 CC (NP). In the method of the invention colostrinin, and its NP are used to  
 CC treat chronic disorders of the central nervous system (CNS), particularly  
 CC neurological and mental disorders such as dementia (Alzheimer's disease);  
 CC motor neurone disease (e.g. Parkinson's disease); psychosis and neurosis  
 CC (including assisting withdrawal from addictive drugs) and the immune  
 CC system, particularly bacterial or viral infections or acquired  
 CC immunological deficiency (e.g. where caused by cancer therapy).  
 CC Colostrinin is a stimulant/modulator of the immune system and may also be  
 CC used as a dietary supplement, e.g. in babies who have not received  
 CC colostrum, young children or adults being given chemotherapy or suffering  
 CC from cachexia due to chronic disease, and to inhibit development of  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 |||||  
 Db 1 VESYVPLFP 9

RESULT 2  
 AAB72529

ID AAB72529 standard; peptide; 9 AA.  
 XX  
 AC AAB72529;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #30.  
 XX  
 KW Dermatological; oxidative stress regulator; colostrinin.



XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022665.  
 XX  
 PR 17-AUG-1999; 99US-0149310P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the cell  
 PT with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations.  
 XX  
 PS Claim 6; Page 26; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 |||||  
 Db 1 VESYVPLFP 9

# RESULT 3

AAB72276

ID AAB72276 standard; peptide; 9 AA.

XX

AC AAB72276;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 31.

XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;

KW central nervous system disorder; neurological disorder; mental disorder;

KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis; infection.

XX

OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022818.  
 XX  
 PR 17-AUG-1999; 99US-0149311P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2001-202804/20.  
 XX  
 PT Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator.  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
 CC have immune response modulatory activity, and are capable of inducing  
 CC cytokines. Colostrinin and its derived peptides are useful for inducing  
 CC cytokine production, for modulating an immunological response and for  
 CC inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies  
 XX  
 SQ Sequence 9 AA;  
  
 Query Match 100.0%; Score 48; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 VESYVPLFP 9  
 |||||  
 Db 1 VESYVPLFP 9  
  
 RESULT 4  
 AAB72561  
 ID AAB72561 standard; peptide; 9 AA.  
 XX  
 AC AAB72561;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #30.  
 XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 22; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 |||||  
 Db 1 VESYVPLFP 9

# RESULT 5

AAO14607

ID AAO14607 standard; peptide; 9 AA.

XX

AC AAO14607;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 30.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers  
 FT Modified-site 9  
 FT /note= "Optional C-terminal amide"  
 XX  
 PN WO200213851-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022777.  
 XX  
 PR 17-AUG-2000; 2000WO-US022777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 7; Page 22; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 |||||  
 Db 1 VESYVPLFP 9

RESULT 6  
 AAM51067  
 ID AAM51067 standard; peptide; 9 AA.  
 XX  
 AC AAM51067;  
 XX  
 DT 30-MAY-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide.  
 XX  
 KW Colostrinin; colostrum; beta-casein; human.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200213849-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022775.  
 XX  
 PR 17-AUG-2000; 2000WO-US022775.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2002-269150/31.  
 XX  
 PT Modulation of blood cell proliferation in a patient involves use of blood  
 PT cell regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Example 1; Page 34; 54pp; English.  
 XX  
 CC The present sequence is that of a colostrinin constituent peptide that  
 CC has been classified as having a beta-casein homologue precursor. The  
 CC peptide has previously been identified as being useful in the treatment  
 CC of disorders of the central nervous system, neurological disorders,  
 CC mental disorders, dementia, neurodegenerative diseases, Alzheimer's  
 CC disease, motor neurone disease, psychosis, neurosis, chronic disorders of  
 CC the immune system, diseases with a bacterial or viral aetiology, and  
 CC acquired immunological deficiencies. The present invention provides  
 CC claimed colistrinin constituted peptides (see AAM51036-66) that are  
 CC useful as immunological regulators and as blood cell regulators. These  
 CC are used in claimed methods of the invention to modulate specific or  
 CC nonspecific immune responses in patients, and to modulate cellular  
 CC proliferation or differentiation of blood cells, such as leucocytes.  
 CC These methods specifically do not use the present colostrinin peptide  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 |||||  
 Db 1 VESYVPLFP 9

RESULT 7  
 AAE20258  
 ID AAE20258 standard; peptide; 9 AA.  
 XX  
 AC AAE20258;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX

DE Colostrinin constituent peptide #30.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnerary.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 9  
 FT /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022776.  
 XX  
 PR 17-AUG-2000; 2000WO-US022776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2002-269151/31.  
 XX  
 PT Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog.  
 XX  
 PS Claim 6; Page 26; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress level  
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
 CC organ, or organism; or for treating oxidative damage to the skin of a  
 CC patient e.g. animal or human; to modulate oxidative stress during/ after  
 CC a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
| | | | | | | |  
Db 1 VESYVPLFP 9

RESULT 8

AAE07189

ID AAE07189 standard; peptide; 8 AA.

XX

AC AAE07189;

XX

DT 06-NOV-2001 (first entry)

XX

DE Colostrinin peptide 5.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;

KW central nervous system disorder; neurodegenerative disorder; weight loss;

KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;

KW acquired immunological deficiency; neurological disorder; dementia;

KW antiviral.

XX

OS Unidentified.

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-488775/53.

XX

PT Peptide useful as an interalia in the treatment of e.g. disorders of the

PT immune system and the central nervous system comprises ten amino-terminal

PT amino acid sequence derived from peptides present in colostrinin.

XX

PS Claim 1; Page 15; 40pp; English.

XX

CC The invention relates to colostrinin peptide fragments which are useful,

CC inter alia, in the treatment of chronic disorders of the immune system

CC and the central nervous system. Colostrinin peptides are used as a

CC medicament in the treatment of neurological disorders e.g., dementia,

CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron

CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and

CC neurosis, in acquired immunological deficiencies, chronic bacterial and

CC viral infections and diseases characterised by the presence of beta-

CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or

CC have suffered from cachexia or weight loss due to the chronic disease.

CC Colostrinin peptides are also used as food additives and as an auxillary

CC withdrawal treatment for drug addicts, after a period of detoxification  
CC and in persons dependent on stimulants. Colostrinin peptides are used to  
CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
CC disturbances of psychiatric patients in a state of depression. These  
CC colostrinin peptides improves the development of immune system in a new  
CC born child and to correct the immunological deficiencies in a child. The  
CC present sequence is colostrinin peptide 5 related to the invention

XX

SQ Sequence 8 AA;

Query Match 91.7%; Score 44; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | | | | | | |  
Db 1 ESYVPLFP 8

# RESULT 9

AAE07199

ID AAE07199 standard; peptide; 9 AA.

XX

AC AAE07199;

XX

DT 06-NOV-2001 (first entry)

XX

DE Modified colostrinin cyclic peptide #5.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
KW central nervous system disorder; neurodegenerative disorder; weight loss;  
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
KW acquired immunological deficiency; neurological disorder; dementia;  
KW antiviral; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic  
FT linkage with Pro found at the C-terminal end"

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-488775/53.

XX



PT Peptide useful as an interalia in the treatment of e.g. disorders of the  
PT immune system and the central nervous system comprises ten amino-terminal  
PT amino acid sequence derived from peptides present in colostrinin.

XX

PS Example 2; Page 9; 40pp; English.

XX

CC The invention relates to colostrinin peptide fragments which are useful,  
CC inter alia, in the treatment of chronic disorders of the immune system  
CC and the central nervous system. Colostrinin peptides are used as a  
CC medicament in the treatment of neurological disorders e.g., dementia,  
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
CC viral infections and diseases characterised by the presence of beta-  
CC amyloid plaques and as a dietary supplement for babies, small children,  
CC adults and senile persons, who have been subjected to chemotherapy or  
CC have suffered from cachexia or weight loss due to the chronic disease.  
CC Colostrinin peptides are also used as food additives and as an auxillary  
CC withdrawal treatment for drug addicts, after a period of detoxification  
CC and in persons dependent on stimulants. Colostrinin peptides are used to  
CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
CC disturbances of psychiatric patients in a state of depression. These  
CC colostrinin peptides improves the development of immune system in a new  
CC born child and to correct the immunological deficiencies in a child. The  
CC present sequence is modified colostrinin cyclic peptide #5 related to the  
CC invention

XX

SQ Sequence 9 AA;

Query Match 91.7%; Score 44; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | | | | | | |  
Db 2 ESYVPLFP 9

#### RESULT 10

ADE12722

ID ADE12722 standard; peptide; 12 AA.

XX

AC ADE12722;

XX

DT 29-JAN-2004 (first entry)

XX

DE Hev b III peptide fragment #1.

XX

KW Allergenic protein; latex ; Hev b III ; allergy ; rubber.

XX

OS Hevea brasiliensis.

XX

PN EP1350797-A1.

XX

PD 08-OCT-2003.

XX

PF 15-SEP-1995; 2003EP-00008977.

XX  
 PR 16-SEP-1994; 94MY-00002468.  
 PR 04-MAY-1995; 95MY-00001205.  
 PR 15-SEP-1995; 95EP-00306534.  
 XX  
 PA (NARP ) RUBBER RES INST MALAYSIA.  
 PA (UYSA-) UNIV SAINS MALAYSIA.  
 XX  
 PI Cardoso MJ, Sharifah H, Samuel-Verghese S, Sunderasan E, Yeang HY;  
 PI Samsidar H;  
 XX  
 DR WPI; 2003-815068/77.  
 XX  
 PT New allergenic protein from latex or tissue of Hevea brasiliensis, useful  
 PT as de-sensitizing agent in treatment of latex protein allergy, and in  
 PT identifying or quantifying antibodies in blood that mediate occurrence of  
 PT an allergic reaction.  
 XX  
 PS Disclosure; Page 9; 36pp; English.  
 XX  
 CC The invention relates to an allergenic protein from the latex or tissue  
 CC of Hevea brasiliensis that is designated Hev b III. Also disclosed are  
 CC internal peptide fragment of Hev b III. The allergenic protein of the  
 CC present invention is useful as de-sensitizing agents in the treatment of  
 CC latex protein allergy. The methods and compositions of the present  
 CC invention are also useful for identifying and/or quantifying antibodies  
 CC in blood or blood products and the level of allergen of natural rubber  
 CC latex present in latex concentrate, manufactured latex products or  
 CC products made from dry rubber that mediate occurrence of an allergic  
 CC reaction induced by natural rubber latex. The current sequence represents  
 CC a peptide fragment of Hev b III produced by tryptic digestion.  
 XX  
 SQ Sequence 12 AA;

Query Match 70.8%; Score 34; DB 7; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 | ||:|| |  
 Db 1 VSSYLPLLP 9

RESULT 11  
 ADE12457  
 ID ADE12457 standard; peptide; 12 AA.  
 XX  
 AC ADE12457;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Hev b III peptide fragment #1.  
 XX  
 KW Allergenic protein; latex; Hev b III; allergy; rubber.  
 XX  
 OS Hevea brasiliensis.  
 XX

PN EP1350798-A1.  
 XX  
 PD 08-OCT-2003.  
 XX  
 PF 15-SEP-1995; 2003EP-00008978.  
 XX  
 PR 16-SEP-1994; 94MY-00002468.  
 PR 04-MAY-1995; 95MY-00001205.  
 PR 15-SEP-1995; 95EP-00306534.  
 XX  
 PA (NARP ) RUBBER RES INST MALAYSIA.  
 PA (UYSA-) UNIV SAINS MALAYSIA.  
 XX  
 PI Cardosa MJ, Sharifah H, Samuel-Verghese S, Sunderasan E, Yeang HY;  
 PI Samsidar H;  
 XX  
 DR WPI; 2003-805965/76.  
 XX  
 PT New allergenic protein of natural rubber latex, useful as de-sensitizing  
 PT agents in the treatment of latex protein allergy, and in identifying or  
 PT quantifying antibodies in blood that mediate occurrence of an allergic  
 PT reaction.  
 XX  
 PS Claim 1; Page 16; 38pp; English.  
 XX  
 CC The invention relates to an allergenic protein from the latex or tissue  
 CC of Hevea brasiliensis that is designated Hev b III. Also disclosed are  
 CC internal peptide fragment of Hev b III. The allergenic protein of the  
 CC present invention is useful as de-sensitizing agents in the treatment of  
 CC latex protein allergy. The methods and compositions of the present  
 CC invention are also useful for identifying and/or quantifying antibodies  
 CC in blood or blood products and the level of allergen of natural rubber  
 CC latex present in latex concentrate, manufactured latex products or  
 CC products made from dry rubber that mediate occurrence of an allergic  
 CC reaction induced by natural rubber latex. The current sequence represents  
 CC a peptide fragment of Hev b III produced by tryptic digestion.  
 XX  
 SQ Sequence 12 AA;

Query Match 70.8%; Score 34; DB 7; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 | ||:| |  
 Db 1 VSSYLPLLP 9

RESULT 12  
 ABR02117

ID ABR02117 standard; peptide; 9 AA.  
 XX  
 AC ABR02117;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 74P3B3 HLA peptide #252.

XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 133; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 9 AA;

Query Match 68.8%; Score 33; DB 6; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 |||||  
 Db 1 VEQYCPWFP 9

RESULT 13  
 ABR02228  
 ID ABR02228 standard; peptide; 10 AA.

XX  
 AC ABR02228;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 74P3B3 HLA peptide #363.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 134; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 10 AA;  
  
 Query Match 68.8%; Score 33; DB 6; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 || || ||

## RESULT 14

ABR02236

ID ABR02236 standard; peptide; 10 AA.

XX

AC ABR02236;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #371.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 134; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 10 AA;

Query Match 68.8%; Score 33; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|||  
Db 2 VEQYCPWFP 10

RESULT 15

ABR01994

ID ABR01994 standard; peptide; 10 AA.

XX

AC ABR01994;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #129.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 132; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 10 AA;

Query Match 68.8%; Score 33; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|| | | |  
Db 2 VEQYCPWFP 10

RESULT 16

ABR02606

ID ABR02606 standard; peptide; 10 AA.

XX

AC ABR02606;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #741.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 138; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.



CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 10 AA;

Query Match 68.8%; Score 33; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|| || ||  
Db 2 VEQYCPWFP 10

RESULT 17

ABR03056

ID ABR03056 standard; peptide; 10 AA.

XX

AC ABR03056;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #1191.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX  
 PS Claim 13; Page 142; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 68.8%; Score 33; DB 6; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 || || ||  
 Db 2 VEQYCPWFP 10

# RESULT 18

ABR02424

ID ABR02424 standard; peptide; 10 AA.

XX

AC ABR02424;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #559.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 136; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 68.8%; Score 33; DB 6; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 || || || ||  
 Db 2 VEQYCPWFP 10

RESULT 19  
 ABP46299

ID ABP46299 standard; peptide; 15 AA.  
 XX  
 AC ABP46299;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human BlyS binding scFv VH CDR3 SEQ ID 2310.  
 XX  
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US019110.

XX  
 PR 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-0277379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX  
 PS Claim 2; Page 2968; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
 CC and so may be used to detect and quantitate the presence of BLyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLyS. They may also be  
 CC administered to treat diseases associated with aberrant BLyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 5; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
 |||||  
 Db 8 SYVPLLP 14

# RESULT 20

ABR30067

ID ABR30067 standard; peptide; 15 AA.

XX

AC ABR30067;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2911.

XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 468; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;  
  
 Query Match 68.8%; Score 33; DB 6; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 1 VESYVPLFP 9  
 || || ||  
 Db 7 VEQYCPWFP 15  
  
 RESULT 21  
 ABR30111  
 ID ABR30111 standard; peptide; 15 AA.

XX  
 AC ABR30111;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 74P3B3 HLA peptide #2955.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 469; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 6; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 || || ||

## RESULT 22

ABR29962

ID ABR29962 standard; peptide; 15 AA.

XX

AC ABR29962;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2806.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 466; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|| || ||  
Db 7 VEQYCPWFP 15

RESULT 23

ABR30102

ID ABR30102 standard; peptide; 15 AA.

XX

AC ABR30102;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2946.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 468; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as .



CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|| || ||  
Db 7 VEQYCPWFP 15

RESULT 24

ABR30015

ID ABR30015 standard; peptide; 15 AA.

XX

AC ABR30015;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2859.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 467; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9  
|| || ||  
Db 5 VEQYCPWFP 13

RESULT 25

ABR30048

ID ABR30048 standard; peptide; 15 AA.

XX

AC ABR30048;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2892.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX  
 PS Claim 13; Page 467; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 6; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9  
 || || ||  
 Db 7 VEQYCPWFP 15

# RESULT 26

ABR29971

ID ABR29971 standard; peptide; 15 AA.

XX

AC ABR29971;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2815.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
PS Claim 13; Page 466; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|| || ||  
Db 4 VEQYCPWFP 12

#### RESULT 27

ABR30004

ID ABR30004 standard; peptide; 15 AA.

XX

AC ABR30004;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2848.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
PS Claim 13; Page 466; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;

Query Match 68.8%; Score 33; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|| | | ||  
Db 1 VEQYCPWFP 9

RESULT 28  
ABP46252  
ID ABP46252 standard; peptide; 16 AA.  
XX  
AC ABP46252;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human BLyS binding scFv VH CDR3 SEQ ID 2263.  
XX  
KW BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.

XX  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US019110.  
 XX  
 PR 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-0277379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX  
 PS Claim 2; Page 2960; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
 CC and so may be used to detect and quantitate the presence of BLyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLyS. They may also be  
 CC administered to treat diseases associated with aberrant BLyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 XX  
 SQ Sequence 16 AA;

Query Match 68.8%; Score 33; DB 5; Length 16;  
 Best Local Similarity 85.7%; Pred. No. 28;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
 |||||  
 Db 8 SYVPLL 14

RESULT 29  
 ABR02132  
 ID ABR02132 standard; peptide; 9 AA.

XX  
 AC ABR02132;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 74P3B3 HLA peptide #267.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 133; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 9 AA;

Query Match 60.4%; Score 29; DB 6; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
 | | | |

## RESULT 30

ABR02528

ID ABR02528 standard; peptide; 9 AA.

XX

AC ABR02528;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #663.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 137; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 9 AA;



Query Match 60.4%; Score 29; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | | |  
Db 1 EQYCPWFP 8

RESULT 31

ABR02946

ID ABR02946 standard; peptide; 9 AA.

XX

AC ABR02946;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #1081.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

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PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 141; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 9 AA;

Query Match 60.4%; Score 29; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ESYVPLFP 9

| | | |

Db 1 EQYCPWFP 8

# RESULT 32

ABR02332

ID ABR02332 standard; peptide; 9 AA.

XX

AC ABR02332;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #467.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 135; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 9 AA;

Query Match 60.4%; Score 29; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | | |  
Db 1 EQYCPWFP 8

### RESULT 33

AAU82797

ID AAU82797 standard; peptide; 10 AA.

XX

AC AAU82797;

XX

DT 23-APR-2002 (first entry)

XX

DE Human Calcitonin targeted peptide #3.

XX

KW Dopamine D2DA; receptor; muscarinic M1; nerve growth factor; calcitonin;

KW human; retro-inverso peptide; physicochemical mode;

KW protein-targeted peptide.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US2002009756-A1.

XX

PD 24-JAN-2002.

XX

PF 23-JAN-2001; 2001US-00767460.

XX

PR 24-JAN-2000; 2000US-00490702.

XX

PA (MAND/) MANDELL A J.

PA (SELZ/) SELZ K A.

PA (SHLE/) SHLESINGER M F.

XX

PI Mandell AJ, Selz KA, Shlesinger MF;

XX

DR WPI; 2002-163853/21.

XX

PT Synthesizing peptides based on matching a physicochemical mode of a  
PT peptide to the same physicochemical mode of a target polypeptide or  
PT protein.

XX  
 PS Example 3; Page 24; 33pp; English.  
 XX  
 CC The invention relates to a method for synthesising a peptide based on  
 CC matching a physicochemical mode of a peptide to the same physicochemical  
 CC mode of a target polypeptide or protein, followed by synthesising a retro  
 CC -inverso peptide version of the peptide comprised of D-amino acids. The  
 CC method is used for designing protein-targeted peptides or peptide  
 CC analogues whose sequences are derived from the target protein sequences  
 CC using target protein sequence, analytically derived templates, and  
 CC relevant distributions of amino acids for weighted random assignments to  
 CC those templates. The protein targets include cell receptors,  
 CC transporters, enzymes, chaperonins, antibodies, surface proteins of  
 CC infectious agents, and any protein involved in protein-protein  
 CC interactions. The method provides an entirely new way of designing  
 CC peptides or peptide analogue molecules capable of binding to and/or  
 CC otherwise modulating the function of protein targets having known amino  
 CC acid sequences. The methods employ three kinds of templates, derived from  
 CC analyses of the target protein sequences, in addition to relevant  
 CC distributions of amino acids, for weighted and constrained random  
 CC assignments to the templates to produce the peptides. The present  
 CC sequence is a peptide derived by the method of the invention targeting  
 CC either the human dopamine D2DA receptor, muscarinic M1 receptor, nerve  
 CC growth factor receptor or calcitonin  
 XX  
 SQ Sequence 10 AA;

Query Match 60.4%; Score 29; DB 5; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 95;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9  
 |::| | ||  
 Db 1 VQTYPPHFP 9

RESULT 34  
 ABR02235  
 ID ABR02235 standard; peptide; 10 AA.  
 XX  
 AC ABR02235;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 74P3B3 HLA peptide #370.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX

PR 10-APR-2001; 2001US-0282739P.  
PR 10-APR-2001; 2001US-0283112P.  
PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX

PS Claim 13; Page 134; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

XX

SQ Sequence 10 AA;

Query Match 60.4%; Score 29; DB 6; Length 10;  
Best Local Similarity 62.5%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | | |  
Db 1 EQYCPWFP 8

RESULT 35

ABR02609

ID ABR02609 standard; peptide; 10 AA.

XX

AC ABR02609;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #744.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 138; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 60.4%; Score 29; DB 6; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
 | | | |  
 Db 1 EQYCPWFP 8

# RESULT 36

ABR02053

ID ABR02053 standard; peptide; 10 AA.

XX

AC ABR02053;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #188.

XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 132; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 60.4%; Score 29; DB 6; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
 | | | |  
 Db 1 EQYCPWFP 8

RESULT 37  
 ABR02387  
 ID ABR02387 standard; peptide; 10 AA.

XX  
 AC ABR02387;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 74P3B3 HLA peptide #522.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX  
 PS Claim 13; Page 136; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 10 AA;  
  
 Query Match 60.4%; Score 29; DB 6; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 2 ESYVPLFP 9  
 | | | | |



Db 1 EQYCPWFP 8

RESULT 38

AAW05005

ID AAW05005 standard; peptide; 13 AA.

XX

AC AAW05005;

XX

DT 03-DEC-1996 (first entry)

XX

DE Peptide related to novel immunomodulators.

XX

KW Immunomodulation; immunomodulator; immune system; anergy; deficiency;

KW aberrant response; chronic bronchitis; atopic disease; AIDS;

KW acquired immune deficiency syndrome; herpes virus infection.

XX

OS Synthetic.

XX

PN WO9611943-A1.

XX

PD 25-APR-1996.

XX

PF 06-OCT-1995; 95WO-SE001151.

XX

PR 14-OCT-1994; 94SE-00003526.

XX

PA (ASTR ) ASTRA AB.

XX

PI Bergstrand H, Eriksson T, Karabelas K, Lindvall M, Saernstrand B;

XX

DR WPI; 1996-221938/22.

XX

PT Peptide(s) with immunomodulatory activity - useful for treating e.g.

PT chronic bronchitis, malignancies, herpes, AIDS or atopic disease, as

PT adjuvants in vaccines, or for inhibiting graft rejection.

XX

PS Claim 1; Page 50; 63pp; English.

XX

CC The present peptide is one of 6 known peptides which concord with a

CC highly generic sequence covering immunomodulatory peptides of 4-15 amino

CC acids being claimed in the present patent application; all 6 peptides are

CC specifically excluded from the claim

XX

SQ Sequence 13 AA;

Query Match 60.4%; Score 29; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9

|:| ||

Db 1 YIPCFP 6

RESULT 39

AAW41667

ID AAW41667 standard; peptide; 13 AA.  
 XX  
 AC AAW41667;  
 XX  
 DT 27-APR-1998 (first entry)  
 XX  
 DE Immunomodulatory peptide.  
 XX  
 KW Immunomodulator; immunosuppressant; immunostimulator; treatment;  
 KW transplant rejection; autoimmune disease; cancer; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9739023-A1.  
 XX  
 PD 23-OCT-1997.  
 XX  
 PF 04-APR-1997; 97WO-SE000574.  
 XX  
 PR 12-APR-1996; 96SE-00001422.  
 PR 23-SEP-1996; 96SE-00003469.  
 XX  
 PA (ASTR ) ASTRA AB.  
 XX  
 PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;  
 XX  
 DR WPI; 1997-526397/48.  
 XX  
 PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)  
 PT which have immuno:stimulatory or immunosuppressive activity - can be used  
 PT to treat, e.g. cancers, infection, auto:immune disease or transplant  
 PT rejection.  
 XX  
 PS Disclosure; Page 19; 183pp; English.  
 XX  
 CC A novel immunosuppressing or immunostimulatory peptide conforms to the  
 CC motifs represented by the formulae of the invention, with the proviso  
 CC that the peptides described in AAW36999, AAW37000 and AAW41647 to  
 CC AAW41682 are excluded. An immunosuppressant can be used to treat  
 CC transplant rejection or autoimmune disease, e.g. rheumatoid arthritis,  
 CC systemic lupus erythematosus, Sjogren's syndrome, scleroderma, mixed  
 CC connective tissue disease, dermatomyositis, polymyositis, Reiter's  
 CC syndrome, Behcet's disease, type I diabetes, Hashimoto's thyroiditis,  
 CC Graves' disease, multiple sclerosis, myasthenia gravis,  
 CC encephalomyelitis, phemphigus vulgaris, vegetans or foliaceus, Senear-  
 CC Usher syndrome or Brazilian phemphigus. An immunostimulator can be used  
 CC to treat conditions such as cancer or infection  
 XX  
 SQ Sequence 13 AA;

Query Match 60.4%; Score 29; DB 2; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVPLFP 9  
 | : | | |  
 Db 1 YIPCFP 6

RESULT 40

AAU17675

ID AAU17675 standard; protein; 13 AA.

XX

AC AAU17675;

XX

DT 07-NOV-2001 (first entry)

XX

DE Novel signal transduction pathway protein, Seq ID 1240.

XX

KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;

KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;

KW immune system disorder; rheumatoid arthritis; inflammatory condition;

KW organ transplant rejection; infection; hepatitis C; blood disorder;

KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;

KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;

KW reproductive system; gastrointestinal; liver disorder; AIDS;

KW acquired immune deficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200154733-A1.

XX

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001312.

XX

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;

XX  
 DR WPI; 2001-465460/50.  
 XX  
 PT Novel polypeptides useful for diagnosing, treating, preventing and/or  
 PT prognosing disorders related to the proteins, including cancers, immune  
 PT disorders and neuronal disorders.  
 XX  
 PS Claim 1; SEQ ID NO 1240; 880pp; English.  
 XX  
 CC The invention relates to novel isolated polypeptides (I), and  
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for  
 CC diagnosing, preventing and treating diseases including immune system  
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
 CC transplant rejections and graft versus host disease, infectious diseases  
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative  
 CC disorders, primary haematopoietic disorders, hyperproliferative disorders  
 CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities  
 CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.  
 CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),  
 CC respiratory disorders, dermatological disorders, in wound healing,  
 CC epithelial cell proliferation, endocrine disorders (e.g. Addison's  
 CC disease), reproductive system disorders, gastrointestinal disorder  
 CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of  
 CC B-cell responsiveness to pathogens, activators of T-cells, to induce  
 CC higher affinity antibodies, and as a means to induce tumour proliferation  
 CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-  
 CC AAU17683 represent novel signal transduction pathway protein, amino acid  
 CC sequences of the invention  
 XX  
 SQ Sequence 13 AA;

Query Match 60.4%; Score 29; DB 4; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
 ||||: |  
 Db 1 SYVPMSP 7

RESULT 41  
 ABO27231  
 ID ABO27231 standard; peptide; 13 AA.  
 XX  
 AC ABO27231;  
 XX  
 DT 10-SEP-2003 (first entry)  
 XX  
 DE Gab3 PXXP motif #3.  
 XX  
 KW Mouse; Gab3; gene therapy; infectious disease; cancer; wound healing;  
 KW neural disorder; immune system disorder; systemic lupus erythematosus;  
 KW rheumatoid arthritis; multiple sclerosis; muscular disorder; sinusitis;  
 KW respiratory disease; nasal vestibulitis; nasal polyp; pulmonary disorder;

KW cardiovascular disorder; congenital heart defect; Ebstein's anomaly;  
KW hypoplastic left heart syndrome; renal disorder; acute kidney failure;  
KW end-stage renal disease; hyperproliferative disorder; Hodgkin's disease;  
KW leukaemia; inflammatory disease; septic shock; bursitis; appendicitis;  
KW allergy; asthma; blood related disorder; thrombosis; atherosclerosis;  
KW myocardial infarction; endocrine disorder; Addison's disease; dysphagia;  
KW corticosteroid deficiency; reproductive system disorder; dysmenorrhea;  
KW testicular atrophy; gastrointestinal disorder; irritable bowel syndrome;  
KW epithelial cell proliferation.

XX  
OS Synthetic.

XX  
PN US2003036505-A1.

XX  
PD 20-FEB-2003.

XX  
PF 20-SEP-2001; 2001US-00955999.

XX  
PR 25-SEP-2000; 2000US-0234997P.

XX  
PA (HUMA-) HUMAN GENOME SCI INC.

XX  
PI Barash SC, Ni J, Ruben SM, Rosen CA, Young PE, Rohrschneider LR;

XX  
DR WPI; 2003-492122/46.

XX  
PT New isolated nucleic acids encoding signal transduction pathway component  
PT polypeptides, useful for diagnosing, treating, and/or preventing  
PT disorders, such as cancer, infections, cardiovascular and inflammatory  
PT diseases.

XX  
PS Disclosure; Page 7; 297pp; English.

XX  
CC The invention relates to an isolated nucleic acid molecule. The methods  
CC and compositions of the present invention are useful for diagnosing,  
CC treating, preventing and/or prognosing disorders related to the novel  
CC polypeptides, such as neural disorders, immune system disorders (e.g.  
CC systemic lupus erythematosus, rheumatoid arthritis, or multiple  
CC sclerosis), muscular disorders, respiratory diseases (e.g. nasal  
CC vestibulitis, nasal polyps, or sinusitis), reproductive disorders,  
CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
CC (e.g. congenital heart defects, Ebstein's anomaly or hypoplastic left  
CC heart syndrome), renal disorders (e.g. acute kidney failure, or end-stage  
CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease or  
CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis, or  
CC appendicitis), allergic reactions and conditions (e.g. asthma), blood  
CC related disorders (e.g. thrombosis, atherosclerosis or myocardial  
CC infarction), endocrine disorders (e.g. Addison's disease or  
CC corticosteroid deficiency), reproductive system disorders (e.g.  
CC testicular atrophy or dysmenorrhea), gastrointestinal disorders (e.g.  
CC dysphagia or irritable bowel syndrome), infectious diseases, and/or  
CC cancerous diseases. The polynucleotides can also be used to aid wound  
CC healing and epithelial cell proliferation. The present sequence  
CC represents the amino acid sequence of a mouse Gab3 domain/motif

XX  
SQ Sequence 13 AA;

Query Match 60.4%; Score 29; DB 6; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
||||: |  
Db 1 SYVPMSP 7

RESULT 42

ADB94383

ID ADB94383 standard; protein; 13 AA.

XX

AC ADB94383;

XX

DT 04-DEC-2003 (first entry)

XX

DE Novel human protein associated polypeptide #4.

XX

KW human; autoimmune disease; Parkinson's disease; silicosis;

KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;

KW immunosuppressive agent; adjuvant; enhance immune response;

KW higher affinity antibody induction;

KW increased serum immunoglobulin concentration.

XX

OS Homo sapiens.

XX

PN US2002168711-A1.

XX

PD 14-NOV-2002.

XX

PF 17-JAN-2001; 2001US-00764868.

XX

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 22-AUG-2000; 2000US-0226868P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.



PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.

XX

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX

PI Rosen CA, Ruben SM, Barash SC;

XX

DR WPI; 2003-719985/68.

XX

PT New isolated polypeptide useful for diagnosing and treating  
PT immunosuppressive conditions such as autoimmune disease and Parkinson's  
PT disease.

XX

PS Disclosure; SEQ ID NO 1240; 345pp; English.

XX

CC The invention relates to an isolated polypeptide. The polypeptide is  
CC useful for diagnosing a pathological condition or a susceptibility to a  
CC pathological condition in a subject, by determining the presence or  
CC amount of expression of the polypeptide in a biological sample and  
CC diagnosing a pathological condition or a susceptibility to a pathological  
CC condition based on the presence or amount of expression of the  
CC polypeptide. The polypeptide is also useful for identifying a binding  
CC partner to the polypeptide, which involves contacting the polypeptide  
CC with a binding partner and determining whether the binding partner  
CC effects an activity of the polypeptide. The polypeptide or the nucleic  
CC acid encoding the polypeptide is useful for preventing, treating, or  
CC ameliorating a medical condition, which involves administering the  
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid  
CC is useful for diagnosing a pathological condition or a susceptibility to  
CC a pathological condition in a subject, which involves determining the  
CC presence or absence of a mutation in The nucleic acid, and diagnosing a

CC pathological condition or susceptibility to a pathological condition  
CC based on the presence or absence of the mutation. The polypeptide, the  
CC nucleic acid and an antibody to the polypeptide are useful for treating  
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal  
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,  
CC the nucleic acid and the antibody are useful as immunosuppressive agents,  
CC as adjuvants to enhance immune responses, and as agents to induce higher  
CC affinity antibodies and increase serum immunoglobulin concentrations. The  
CC present sequence represents the amino acid sequence of a novel human  
CC protein associated polypeptide. Note: The sequence data for this patent  
CC did not form part of the printed specification but was obtained in  
CC electronic format direct from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20020168711.

XX

SQ Sequence 13 AA;

Query Match 60.4%; Score 29; DB 7; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9

||||: |

Db 1 SYVPMSP 7

RESULT 43

AAP80629

ID AAP80629 standard; protein; 14 AA.

XX

AC AAP80629;

XX

DT 25-MAR-2003 (revised)

DT 17-SEP-1990 (first entry)

XX

DE Synthetic hydrophobic surfactant-associated protein (SAP) (Val) peptide.

XX

KW Synthetic hydrophobic surfactant-associated protein (SAP) (Val);

KW hyaline membrane disease (HMD) prevention; assays.

XX

OS Homo sapiens.

XX

PN WO8803170-A.

XX

PD 05-MAY-1988.

XX

PF 02-OCT-1987; 87WO-US002536.

XX

PR 24-OCT-1986; 86WO-US002258.

PR 08-DEC-1986; 86US-00939206.

PR 10-JUN-1987; 87US-00060719.

PR 01-OCT-1987; 87US-00101680.

PR 03-DEC-1987; 87WO-US003180.

XX

PA (WHIT/) WHITSETT J A.

PA (ABBO ) ABBOTT LAB.

XX

PI Whitsett JA, Fox JL, Pilotmatia TJ, Meuth JL, Sarin VK;

XX  
 DR WPI; 1988-133244/19.  
 XX  
 PT Pulmonary hydrophobic surfactant-associated proteins - used with lipid(s)  
 PT to treat and prevent hyaline membrane disease and similar syndromes.  
 XX  
 PS Claim 8; Page 83; 144pp; English.  
 XX  
 CC It can be made by chemical or enzymatic peptide synthesis. Also claimed  
 CC is a purified and isolated DNA sequence encoding SAP (Val). SAP (Val) and  
 CC SAP (Phe), when combined with lipids, have significant pulmonary  
 CC biophysical surfactant activity that may be utilised to treat and prevent  
 CC hyaline membrane disease (HMD) and other syndromes associated with lack  
 CC or insufficient amts. of natural pulmonary surfactant material.  
 CC Antibodies and antisera may also be made which are directed against SAP  
 CC (Val) or SAP (Phe). SAP (Val) and SAP (Phe) in body fluids may be assayed  
 CC using the compsns. (Updated on 25-MAR-2003 to correct PR field.) (Updated  
 CC on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct  
 CC PI field.)  
 XX  
 SQ Sequence 14 AA;

Query Match 60.4%; Score 29; DB 1; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 | : | | |  
 Db 1 YIPCFP 6

# RESULT 44

AAW05004

ID AAW05004 standard; peptide; 14 AA.

XX

AC AAW05004;

XX

DT 03-DEC-1996 (first entry)

XX

DE Peptide related to novel immunomodulators.

XX

KW Immunomodulation; immunomodulator; immune system; anergy; deficiency;

KW aberrant response; chronic bronchitis; atopic disease; AIDS;

KW acquired immune deficiency syndrome; herpes virus infection.

XX

OS Synthetic.

XX

PN W09611943-A1.

XX

PD 25-APR-1996.

XX

PF 06-OCT-1995; 95WO-SE001151.

XX

PR 14-OCT-1994; 94SE-00003526.

XX

PA (ASTR ) ASTRA AB.

XX

PI Bergstrand H, Eriksson T, Karabelas K, Lindvall M, Saernstrand B;  
 XX  
 DR WPI; 1996-221938/22.  
 XX  
 PT Peptide(s) with immunomodulatory activity - useful for treating e.g.  
 PT chronic bronchitis, malignancies, herpes, AIDS or atopic disease, as  
 PT adjuvants in vaccines, or for inhibiting graft rejection.  
 XX  
 PS Claim 1; Page 50; 63pp; English.  
 XX  
 CC The present peptide is one of 6 known peptides which concord with a  
 CC highly generic sequence covering immunomodulatory peptides of 4-15 amino  
 CC acids being claimed in the present patent application; all 6 peptides are  
 CC specifically excluded from the claim  
 XX  
 SQ Sequence 14 AA;

Query Match 60.4%; Score 29; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVPLEP 9  
 | : | | |  
 Db 1 YIPCFP 6

#### RESULT 45

AAW41666

ID AAW41666 standard; peptide; 14 AA.

XX

AC AAW41666;

XX

DT 27-APR-1998 (first entry)

XX

DE Immunomodulatory peptide.

XX

KW Immunomodulator; immunosuppressant; immunostimulator; treatment;  
 KW transplant rejection; autoimmune disease; cancer; infection.

XX

OS Synthetic.

XX

PN WO9739023-A1.

XX

PD 23-OCT-1997.

XX

PF 04-APR-1997; 97WO-SE000574.

XX

PR 12-APR-1996; 96SE-00001422.

PR 23-SEP-1996; 96SE-00003469.

XX

PA (ASTR ) ASTRA AB.

XX

PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;

XX

DR WPI; 1997-526397/48.

XX

PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)

PT which have immuno:stimulatory or immunosuppressive activity - can be used  
PT to treat, e.g. cancers, infection, auto:immune disease or transplant  
PT rejection.

XX

PS Disclosure; Page 19; 183pp; English.

XX

CC A novel immunosuppressing or immunostimulatory peptide conforms to the  
CC motifs represented by the formulae of the invention, with the proviso  
CC that the peptides described in AAW36999, AAW37000 and AAW41647 to  
CC AAW41682 are excluded. An immunosuppressant can be used to treat  
CC transplant rejection or autoimmune disease, e.g. rheumatoid arthritis,  
CC systemic lupus erythematosus, Sjogren's syndrome, scleroderma, mixed  
CC connective tissue disease, dermatomyositis, polymyositis, Reiter's  
CC syndrome, Behcet's disease, type I diabetes, Hashimoto's thyroiditis,  
CC Graves' disease, multiple sclerosis, myasthenia gravis,  
CC encephalomyelitis, pemphigus vulgaris, vegetans or foliaceus, Senear-  
CC Usher syndrome or Brazilian pemphigus. An immunostimulator can be used  
CC to treat conditions such as cancer or infection

XX

SQ Sequence 14 AA;

Query Match 60.4%; Score 29; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9

|:| ||

Db 1 YIPCFP 6

#### RESULT 46

ABP46646

ID ABP46646 standard; peptide; 14 AA.

XX

AC ABP46646;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human BLyS binding scFv VH CDR3 SEQ ID 2657.

XX

KW BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

OS Homo sapiens.

XX

PN WO200202641-A1.

XX

PD 10-JAN-2002.

XX

PF 15-JUN-2001; 2001WO-US019110.

XX

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-0277379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX  
 PS Claim 2; Page 3027; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
 CC and so may be used to detect and quantitate the presence of BLyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLyS. They may also be  
 CC administered to treat diseases associated with aberrant BLyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 XX  
 SQ Sequence 14 AA;

Query Match 60.4%; Score 29; DB 5; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 | |||  
 Db 9 YSPLFP 14

# RESULT 47

AAU82854

ID AAU82854 standard; peptide; 10 AA.

XX

AC AAU82854;

XX

DT 23-APR-2002 (first entry)

XX

DE Human Calcitonin targeted peptide #60.

XX

KW Dopamine D2DA; receptor; muscarinic M1; nerve growth factor; calcitonin;

KW human; retro-inverso peptide; physicochemical mode;

KW protein-targeted peptide.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US2002009756-A1.  
 XX  
 PD 24-JAN-2002.  
 XX  
 PF 23-JAN-2001; 2001US-00767460.  
 XX  
 PR 24-JAN-2000; 2000US-00490702.  
 XX  
 PA (MAND/) MANDELL A J.  
 PA (SELZ/) SELZ K A.  
 PA (SHLE/) SHLESINGER M F.  
 XX  
 PI Mandell AJ, Selz KA, Shlesinger MF;  
 XX  
 DR WPI; 2002-163853/21.  
 XX  
 PT Synthesizing peptides based on matching a physicochemical mode of a  
 PT peptide to the same physicochemical mode of a target polypeptide or  
 PT protein.  
 XX  
 PS Example 3; Page 24; 33pp; English.  
 XX  
 CC The invention relates to a method for synthesising a peptide based on  
 CC matching a physicochemical mode of a peptide to the same physicochemical  
 CC mode of a target polypeptide or protein, followed by synthesising a retro  
 CC -inverso peptide version of the peptide comprised of D-amino acids. The  
 CC method is used for designing protein-targeted peptides or peptide  
 CC analogues whose sequences are derived from the target protein sequences  
 CC using target protein sequence, analytically derived templates, and  
 CC relevant distributions of amino acids for weighted random assignments to  
 CC those templates. The protein targets include cell receptors,  
 CC transporters, enzymes, chaperonins, antibodies, surface proteins of  
 CC infectious agents, and any protein involved in protein-protein  
 CC interactions. The method provides an entirely new way of designing  
 CC peptides or peptide analogue molecules capable of binding to and/or  
 CC otherwise modulating the function of protein targets having known amino  
 CC acid sequences. The methods employ three kinds of templates, derived from  
 CC analyses of the target protein sequences, in addition to relevant  
 CC distributions of amino acids, for weighted and constrained random  
 CC assignments to the templates to produce the peptides. The present  
 CC sequence is a peptide derived by the method of the invention targeting  
 CC either the human dopamine D2DA receptor, muscarinic M1 receptor, nerve  
 CC growth factor receptor or calcitonin  
 XX  
 SQ Sequence 10 AA;

Query Match 58.3%; Score 28; DB 5; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
 || | ||

## RESULT 48

AAW39045

ID AAW39045 standard; peptide; 17 AA.

XX

AC AAW39045;

XX

DT 27-MAR-1998 (first entry)

XX

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:446.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;

KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;

KW PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US002298.

XX

PR 16-FEB-1996; 96US-00602999.

XX

PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX

PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JE;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src tyrosine  
PT kinase(s) and to stimulate immune response by increasing production of  
PT certain lymphokine(s), e.g. interleukin-1.

XX

PS Claim 22; Page 94; 131pp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology  
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain  
CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which  
CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain  
CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides  
CC can be used in the method to identify inhibitors of their binding to  
CC their respective SH3 domains, which could be used to modulate the  
CC pharmacological activity of proteins or polypeptide containing the SH3  
CC domain. The peptides can also be used to activate Src or Src-related  
CC protein tyrosine kinases, to stimulate the immune response by increasing  
CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
CC and interleukin-1, or to deliver a conjugated molecule to certain



CC cellular compartments containing Src or Src related proteins  
XX  
SQ Sequence 17 AA;

Query Match 58.3%; Score 28; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | : | : |  
Db 6 EWYIPIIP 13

RESULT 49

AAE18839

ID AAE18839 standard; peptide; 11 AA.

XX

AC AAE18839;

XX

DT 17-MAY-2002 (first entry)

XX

DE Human calreticulin N-domain motif #1.

XX

KW Human; prostate cancer; calreticulin; TID-1 protein; TRAITS protein;  
KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;  
KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy; U19;  
KW N domain; cytostatic.

XX

OS Homo sapiens.

XX

PN WO200206327-A2.

XX

PD 24-JAN-2002.

XX

PF 17-JUL-2001; 2001WO-US022357.

XX

PR 17-JUL-2000; 2000US-0218761P.

PR 16-JUL-2001; 2001US-00906393.

XX

PA (NOUN ) UNIV NORTHWESTERN.

XX

PI Wang Z, Xiao W;

XX

DR WPI; 2002-179780/23.

XX

PT Identifying a subject that is likely to have aggressive form of prostate  
PT cancer, involves comparing calreticulin levels in prostate specimen of  
PT the subject and in benign prostatic epithelial cells of the same subject.

XX

PS Example 2; Page 83; 148pp; English.

XX

CC The present invention relates to methods of distinguishing aggressive  
CC forms of prostate cancer from non-aggressive forms. The method involves  
CC comparing the level of calreticulin in prostate specimen and in benign  
CC prostatic epithelial cells of a subject. The invention particularly  
CC relates to two proteins, namely calreticulin and TID-1 (TRAITS; U19) that  
CC are down-regulated in aggressive forms of prostate cancer but not in

CC slowly progressing prostate cancer. They play important roles in the part  
CC of androgen action pathway that suppresses cell proliferation and/or  
CC prevents prostate cancer. The method is useful for identifying a subject  
CC who is likely to have an aggressive form of prostate cancer. The  
CC invention further relates to a method of identifying a subject with a  
CC slow growing form of prostate cancer. TID-1 sequences are useful for  
CC treating cancers such as epithelium-derived carcinomas, kidney cancers,  
CC lymphomas, leukaemias and prostate cancers. Sequences of the invention  
CC are used as vaccines and in gene therapy. The present peptide sequence is  
CC human calreticulin N domain motif which interacts with integrin alpha  
XX  
SQ Sequence 11 AA;

Query Match 56.2%; Score 27; DB 5; Length 11;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|| |||  
Db 5 YVKLFP 10

RESULT 50

ABR58779

ID ABR58779 standard; peptide; 12 AA.

XX

AC ABR58779;

XX

DT 11-JUL-2003 (first entry)

XX

DE Alzheimer's Disease-associated protein isoform, API-384, SEQ ID 304.

XX

KW Nootropic; Neuroprotective; Alzheimer's disease; API; human;

KW Alzheimer's Disease-associated protein isoform.

XX

OS Homo sapiens.

XX

PN WO2003028543-A2.

XX

PD 10-APR-2003.

XX

PF 03-OCT-2002; 2002WO-US031642.

XX

PR 03-OCT-2001; 2001US-0326708P.

XX

PA (PFIZ ) PFIZER PROD INC.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Durham LK, Friedman DL, Herath HMA, Kimmel LH, Parekh RB;

PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;

PI Sunderland PT, Townsend RR, White WF, Williams SA;

XX

DR WPI; 2003-371957/35.

XX

PT Screening or diagnosing of Alzheimer's disease (AD) determine the stage

PT or severity of AD in a subject, comprises analyzing a test sample of body

PT fluid from the subject by 2-dimensional electrophoresis.

XX

PS Claim 2; Page 33; 179pp; English.

XX

CC The present invention relates to methods for screening or diagnosing  
CC Alzheimer's disease (AD) to determine the stage or severity of AD in a  
CC subject, to identify subject at risk of developing AD, or to monitor the  
CC effect of therapy administered. The methods comprise analysing a test  
CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-  
CC dimensional array of AD-associated features (AFs). The method  
CC alternatively comprises quantitatively detecting in a sample of body  
CC fluid from the subject, one or more AD-associated protein isoforms (APIs;  
CC ABR58710-ABR59184)

XX

SQ Sequence 12 AA;

Query Match 56.2%; Score 27; DB 6; Length 12;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VESYVP 6  
| | | | |  
Db 2 VESYTP 7

Search completed: July 4, 2004, 04:40:59  
Job time : 24.0896 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 5.64179 Seconds  
 (without alignments)  
 82.356 Million cell updates/sec

Title: US-09-641-802-31  
 Perfect score: 48  
 Sequence: 1 VESYVPLFP 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7  
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	48	100.0	9	4	US-09-641-803-31	Sequence 31, Appl
2	29	60.4	10	4	US-09-490-702B-64	Sequence 64, Appl
3	29	60.4	13	3	US-08-836-480-37	Sequence 37, Appl
4	29	60.4	13	3	US-09-562-897-37	Sequence 37, Appl
5	29	60.4	14	3	US-08-836-480-36	Sequence 36, Appl
6	29	60.4	14	3	US-09-562-897-36	Sequence 36, Appl
7	28	58.3	10	4	US-09-490-702B-93	Sequence 93, Appl
8	28	58.3	17	3	US-08-602-999A-446	Sequence 446, App
9	28	58.3	17	3	US-08-602-999A-447	Sequence 447, App
10	28	58.3	17	4	US-09-500-124-446	Sequence 446, App
11	28	58.3	17	4	US-09-500-124-447	Sequence 447, App

12	26	54.2	11	3	US-08-960-190A-30	Sequence 30, Appl
13	26	54.2	17	6	5223424-4	Patent No. 5223424
14	25	52.1	10	3	US-08-159-339A-1151	Sequence 1151, Ap
15	25	52.1	11	1	US-07-906-349A-12	Sequence 12, Appl
16	25	52.1	11	1	US-08-167-035-12	Sequence 12, Appl
17	25	52.1	11	1	US-08-208-887A-12	Sequence 12, Appl
18	25	52.1	11	2	US-08-539-005-12	Sequence 12, Appl
19	25	52.1	11	3	US-08-652-877-69	Sequence 69, Appl
20	25	52.1	11	3	US-08-476-515A-69	Sequence 69, Appl
21	25	52.1	11	4	US-09-280-598-12	Sequence 12, Appl
22	25	52.1	15	3	US-08-602-999A-379	Sequence 379, App
23	25	52.1	15	4	US-09-500-124-379	Sequence 379, App
24	25	52.1	16	4	US-08-213-419B-7	Sequence 7, Appli
25	25	52.1	17	4	US-09-060-299-403	Sequence 403, App
26	25	52.1	17	4	US-09-402-923A-403	Sequence 403, App
27	24	50.0	7	2	US-08-837-593-13	Sequence 13, Appl
28	24	50.0	9	4	US-09-266-764-16	Sequence 16, Appl
29	24	50.0	10	1	US-08-066-299-3	Sequence 3, Appli
30	24	50.0	10	1	US-08-362-232-3	Sequence 3, Appli
31	24	50.0	10	1	US-08-265-047-7	Sequence 7, Appli
32	24	50.0	10	1	US-08-814-196-3	Sequence 3, Appli
33	24	50.0	10	2	US-08-630-645-10	Sequence 10, Appl
34	24	50.0	10	4	US-08-766-596A-10	Sequence 10, Appl
35	24	50.0	10	5	PCT-US96-10220-10	Sequence 10, Appl
36	24	50.0	11	1	US-08-066-299-1	Sequence 1, Appli
37	24	50.0	11	1	US-08-128-971B-6	Sequence 6, Appli
38	24	50.0	11	1	US-08-265-047-5	Sequence 5, Appli
39	24	50.0	11	3	US-08-652-877-50	Sequence 50, Appl
40	24	50.0	11	3	US-08-476-515A-50	Sequence 50, Appl
41	24	50.0	12	3	US-08-318-794-1	Sequence 1, Appli
42	24	50.0	12	4	US-08-470-106-1	Sequence 1, Appli
43	24	50.0	13	1	US-08-408-604A-37	Sequence 37, Appl
44	24	50.0	13	5	PCT-US93-09626-37	Sequence 37, Appl
45	24	50.0	14	1	US-08-103-490A-23	Sequence 23, Appl
46	24	50.0	14	1	US-08-103-490A-40	Sequence 40, Appl
47	24	50.0	15	3	US-08-602-999A-319	Sequence 319, App
48	24	50.0	15	3	US-08-743-168B-26	Sequence 26, Appl
49	24	50.0	15	3	US-08-743-168B-27	Sequence 27, Appl
50	24	50.0	15	4	US-09-500-124-319	Sequence 319, App
51	24	50.0	15	5	PCT-US96-10435-26	Sequence 26, Appl
52	24	50.0	15	5	PCT-US96-10435-27	Sequence 27, Appl
53	24	50.0	16	1	US-08-408-604A-26	Sequence 26, Appl
54	24	50.0	16	5	PCT-US93-09626-26	Sequence 26, Appl
55	24	50.0	17	3	US-08-318-794-23	Sequence 23, Appl
56	24	50.0	17	4	US-08-470-106-23	Sequence 23, Appl
57	24	50.0	18	3	US-08-602-999A-305	Sequence 305, App
58	24	50.0	18	4	US-09-500-124-305	Sequence 305, App
59	23.5	49.0	11	4	US-09-341-982-12	Sequence 12, Appl
60	23	47.9	8	2	US-08-934-222-140	Sequence 140, App
61	23	47.9	8	2	US-08-933-402-140	Sequence 140, App
62	23	47.9	8	2	US-09-207-621-140	Sequence 140, App
63	23	47.9	8	2	US-08-532-818-140	Sequence 140, App
64	23	47.9	8	3	US-09-231-797-140	Sequence 140, App
65	23	47.9	8	3	US-08-934-224-140	Sequence 140, App
66	23	47.9	8	3	US-08-933-843-140	Sequence 140, App
67	23	47.9	8	3	US-08-934-223-140	Sequence 140, App
68	23	47.9	8	3	US-09-413-492-140	Sequence 140, App

69	23	47.9	10	1	US-08-128-971B-4	Sequence 4, Appli
70	23	47.9	11	1	US-08-066-299-5	Sequence 5, Appli
71	23	47.9	11	1	US-08-265-047-9	Sequence 9, Appli
72	23	47.9	11	3	US-08-652-877-40	Sequence 40, Appl
73	23	47.9	11	3	US-08-652-877-49	Sequence 49, Appl
74	23	47.9	11	3	US-08-476-515A-40	Sequence 40, Appl
75	23	47.9	11	3	US-08-476-515A-49	Sequence 49, Appl
76	23	47.9	12	3	US-09-385-442-34	Sequence 34, Appl
77	23	47.9	14	1	US-08-290-448A-10	Sequence 10, Appl
78	23	47.9	14	1	US-08-290-448A-10	Sequence 10, Appl
79	23	47.9	14	1	US-08-175-069A-10	Sequence 10, Appl
80	23	47.9	14	4	US-08-461-939B-10	Sequence 10, Appl
81	23	47.9	14	4	US-08-464-000-10	Sequence 10, Appl
82	23	47.9	15	1	US-08-408-604A-24	Sequence 24, Appl
83	23	47.9	15	4	US-09-170-769A-19	Sequence 19, Appl
84	23	47.9	15	5	PCT-US93-09626-24	Sequence 24, Appl
85	23	47.9	16	1	US-08-185-432-14	Sequence 14, Appl
86	23	47.9	16	4	US-08-732-749-7	Sequence 7, Appli
87	23	47.9	16	4	US-09-715-923-8	Sequence 8, Appli
88	22	45.8	7	3	US-09-081-180-12	Sequence 12, Appl
89	22	45.8	7	3	US-09-040-786-12	Sequence 12, Appl
90	22	45.8	7	3	US-09-118-408-26	Sequence 26, Appl
91	22	45.8	7	4	US-09-209-525-25	Sequence 25, Appl
92	22	45.8	7	4	US-09-506-855-26	Sequence 26, Appl
93	22	45.8	7	4	US-09-911-176B-26	Sequence 26, Appl
94	22	45.8	7	4	US-09-552-225A-17	Sequence 17, Appl
95	22	45.8	7	4	US-09-619-740-26	Sequence 26, Appl
96	22	45.8	7	4	US-09-506-852-26	Sequence 26, Appl
97	22	45.8	7	4	US-09-552-204A-17	Sequence 17, Appl
98	22	45.8	8	1	US-08-178-570-47	Sequence 47, Appl
99	22	45.8	8	1	US-08-408-604A-200	Sequence 200, App
100	22	45.8	8	1	US-08-408-604A-201	Sequence 201, App

#### ALIGNMENTS

##### RESULT 1

US-09-641-803-31

; Sequence 31, Application US/09641803

; Patent No. 6500798

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

; FILE REFERENCE: 265.00220101

; CURRENT APPLICATION NUMBER: US/09/641,803

; CURRENT FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 31

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-31

Query Match 100.0%; Score 48; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
| | | | | | | |  
Db 1 VESYVPLFP 9

#### RESULT 2

US-09-490-702B-64

; Sequence 64, Application US/09490702B  
; Patent No. 6560542  
; GENERAL INFORMATION:  
; APPLICANT: Mandell, Arnold  
; APPLICANT: Selz, Karen  
; APPLICANT: Shlesinger, Michael  
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or  
Modulation of the  
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
; FILE REFERENCE: 01561-0002-00US00  
; CURRENT APPLICATION NUMBER: US/09/490,702B  
; CURRENT FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 64  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: synthetic  
US-09-490-702B-64

Query Match 60.4%; Score 29; DB 4; Length 10;  
Best Local Similarity 55.6%; Pred. No. 26;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
| : | | |  
Db 1 VQTYPPHFP 9

#### RESULT 3

US-08-836-480-37

; Sequence 37, Application US/08836480  
; Patent No. 6103697  
; GENERAL INFORMATION:  
; APPLICANT: Bergstrand, Hakan  
; APPLICANT: Erickson, Tomas  
; APPLICANT: Karabelas, Kostas

```

; APPLICANT: Lindvall, Magnus
; APPLICANT: Sarnstrand, Bengt
; TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,480
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 95\403256-8
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06275/036001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-480-37

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Query Match          60.4%; Score 29; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 34;
Matches      4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      4 YVPLFP 9
        |:| ||
Db      1 YIPCFP 6

```

```

RESULT 4
US-09-562-897-37
; Sequence 37, Application US/09562897
; Patent No. 6228374
; GENERAL INFORMATION:
; APPLICANT: Bergstrand, Hakan
; Erickson, Tomas
; Karabelas, Kostas
; Lindvall, Magnus
; Sarnstrand, Bengt

```



```

; TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/562,897
; FILING DATE: 01-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,480
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06275/036001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-562-897-37

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```

Query Match          60.4%; Score 29; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 34;
Matches    4; Conservative    1; Mismatches    1; Indels    0; Gaps    0;

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```

Qy      4 YVPLFP 9
        |:| ||
Db      1 YIPCFP 6

```

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RESULT 5
US-08-836-480-36
; Sequence 36, Application US/08836480
; Patent No. 6103697
; GENERAL INFORMATION:
; APPLICANT: Bergstrand, Hakan
; APPLICANT: Erickson, Tomas
; APPLICANT: Karabelas, Kostas
; APPLICANT: Lindvall, Magnus
; APPLICANT: Sarnstrand, Bengt
; TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS

```

```

; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,480
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 95\403256-8
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06275/036001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-480-36

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Query Match          60.4%; Score 29; DB 3; Length 14;
Best Local Similarity 66.7%; Pred. No. 36;
Matches    4; Conservative    1; Mismatches    1; Indels    0; Gaps    0;

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Qy      4 YVPLFP 9
        |:| ||
Db      1 YIPCFP 6

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# RESULT 6

US-09-562-897-36

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; Sequence 36, Application US/09562897
; Patent No. 6228374

```

## GENERAL INFORMATION:

```

; APPLICANT: Bergstrand, Hakan
; Erickson, Tomas
; Karabelas, Kostas
; Lindvall, Magnus
; Sarnstrand, Bengt

```

```

; TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Fish & Richardson, P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/562,897  
 ; FILING DATE: 01-May-2000  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/836,480  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fraser, Janis K.  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 06275/036001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-542-5070  
 ; TELEFAX: 617-542-8906  
 ; INFORMATION FOR SEQ ID NO: 36:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
 US-09-562-897-36

Query Match 60.4%; Score 29; DB 3; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 36;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVPLFP 9  
 | : | | |  
 Db 1 YIPCFP 6

RESULT 7  
 US-09-490-702B-93  
 ; Sequence 93, Application US/09490702B  
 ; Patent No. 6560542  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mandell, Arnold  
 ; APPLICANT: Selz, Karen  
 ; APPLICANT: Shlesinger, Michael  
 ; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or  
 Modulation of the  
 ; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
 ; FILE REFERENCE: 01561-0002-00US00  
 ; CURRENT APPLICATION NUMBER: US/09/490,702B  
 ; CURRENT FILING DATE: 2000-01-24

; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: synthetic  
US-09-490-702B-93

Query Match 58.3%; Score 28; DB 4; Length 10;  
Best Local Similarity 71.4%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
|| | ||  
Db 3 SYTPEFP 9

RESULT 8

US-08-602-999A-446

; Sequence 446, Application US/08602999A  
; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 446:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-446

Query Match 58.3%; Score 28; DB 3; Length 17;  
Best Local Similarity 50.0%; Pred. No. 68;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | : | : |  
Db 6 EWYIPIIP 13

RESULT 9

US-08-602-999A-447

; Sequence 447, Application US/08602999A  
; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 447:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-447

Query Match 58.3%; Score 28; DB 3; Length 17;  
Best Local Similarity 50.0%; Pred. No. 68;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | : | : |  
Db 6 EWYIPIIP 13

RESULT 10

US-09-500-124-446

; Sequence 446, Application US/09500124  
; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 446:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-446

Query Match 58.3%; Score 28; DB 4; Length 17;  
Best Local Similarity 50.0%; Pred. No. 68;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | : | : |  
Db 6 EWYIPIIP 13

RESULT 11

US-09-500-124-447

; Sequence 447, Application US/09500124  
; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 447:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-447

Query Match 58.3%; Score 28; DB 4; Length 17;  
Best Local Similarity 50.0%; Pred. No. 68;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| |:|: |  
Db 6 EWYIPIIP 13

RESULT 12

US-08-960-190A-30  
; Sequence 30, Application US/08960190A  
; Patent No. 6232445  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; APPLICANT: Acevedo, Jorge  
; APPLICANT: Burkhardt, Martin  
; APPLICANT: Jiao, Jin-an  
; APPLICANT: Wong, Hing C.  
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: usa  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/960,190A  
; FILING DATE: 29-OCT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860



; REFERENCE/DOCKET NUMBER: 48002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-960-190A-30

Query Match 54.2%; Score 26; DB 3; Length 11;  
Best Local Similarity 50.0%; Pred. No. 98;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
| | : | |  
Db 3 EEYMPMEP 10

RESULT 13  
5223424-4  
;Patent No. 5223424  
; APPLICANT: COCHRAN, MARK;CHIANG, CHRISTINA H.;MACDONALD,  
;RICHARD D.  
; TITLE OF INVENTION: ATTENUATED HERPESVIRUSES AND  
;HERPESVIRUSES WHICH INCLUDE FOREIGN DNA ENCODING AN AMINO  
;ACID SEQUENCE  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/225,032  
; FILING DATE: 27-JUL-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 78,519  
; FILING DATE: 27-JUL-1987  
; APPLICATION NUMBER: 933,107  
; FILING DATE: 20-NOV-1986  
; APPLICATION NUMBER: 902,887  
; FILING DATE: 02-SEP-1986  
; APPLICATION NUMBER: 887,140  
; FILING DATE: 17-JUL-1986  
; APPLICATION NUMBER: 823,102  
; FILING DATE: 27-JAN-1986  
; APPLICATION NUMBER: 773,430  
; FILING DATE: 06-SEP-1985  
;SEQ ID NO:4:  
; LENGTH: 17  
5223424-4

Query Match 54.2%; Score 26; DB 6; Length 17;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9

Db                    || : || |  
                      5 VEQHNPLIP 13

RESULT 14

US-08-159-339A-1151

; Sequence 1151, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Celis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A

; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666

; FILING DATE: 07-AUG-1992

; APPLICATION NUMBER: US 08/027,746

; FILING DATE: 05-MAR-1993

; APPLICATION NUMBER: US 08/103,396

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; TELEX:

; INFORMATION FOR SEQ ID NO: 1151:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-159-339A-1151

Query Match

52.1%; Score 25; DB 3; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
|||:|  
Db 2 VPLYP 6

RESULT 15

US-07-906-349A-12

; Sequence 12, Application US/07906349A

; Patent No. 5434064

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph

; APPLICANT: Skolnik, Edward Y.

; APPLICANT: Margolis, Benjamin L.

; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE  
KINASES AND

; TITLE OF INVENTION: TARGET PROTEINS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/906,349A

; FILING DATE: 30-JUN-1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/643,237

; FILING DATE: 18-JAN-1991

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-906-349A-12

Query Match 52.1%; Score 25; DB 1; Length 11;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVPL 7

Db                    | |||:  
                      4 EYVPM 9

RESULT 16

US-08-167-035-12

; Sequence 12, Application US/08167035

; Patent No. 5618691

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph

; APPLICANT: Skolnick, Edward Y.

; APPLICANT: Margolis, Benjamin L.

; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE

; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: 10036-2711

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/167,035

; FILING DATE: 16-DEC-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7683-062

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 6

; OTHER INFORMATION: /label= A

; OTHER INFORMATION: /note= "The tyrosine is phosphorylated."

US-08-167-035-12

Query Match                    52.1%; Score 25; DB 1; Length 11;

Best Local Similarity       66.7%; Pred. No. 1.5e+02;

Matches       4; Conservative       1; Mismatches       1; Indels       0; Gaps       0;

Qy 2 ESYVPL 7  
| |||:  
Db 4 EEYVPM 9

RESULT 17

US-08-208-887A-12

; Sequence 12, Application US/08208887A

; Patent No. 5677421

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph

; APPLICANT: Skolnick, Edward Y.

; APPLICANT: Margolis, Benjamin L.

; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE

; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: 10036-2711

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/208,887A

; FILING DATE: 11-MAR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7683-063

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 6

; OTHER INFORMATION: /label= A

; OTHER INFORMATION: /note= "The tyrosine is phosphorylated."

US-08-208-887A-12

Query Match 52.1%; Score 25; DB 1; Length 11;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVPL 7  
| |||:  
Db 4 EEYVPM 9

RESULT 18

US-08-539-005-12

; Sequence 12, Application US/08539005  
; Patent No. 5858686  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Skolnick, Edward Y.  
; APPLICANT: Margolis, Benjamin L.  
; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR  
; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE  
; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: 10036-2711  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/539,005  
; FILING DATE: 4-OCT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/167,035  
; FILING DATE: 16-DEC-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-062  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /label= A  
; OTHER INFORMATION: /note= "The tyrosine is phosphorylated."

US-08-539-005-12

Query Match 52.1%; Score 25; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVPL 7  
| | | :  
Db 4 EEYVPM 9

RESULT 19

US-08-652-877-69

; Sequence 69, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalm, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314

; FILING DATE: 07-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355E-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-652-877-69

Query Match 52.1%; Score 25; DB 3; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVPL 7  
| |||:  
Db 4 EEYVPM 9

RESULT 20

US-08-476-515A-69

; Sequence 69, Application US/08476515A  
; Patent No. 6239270

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran  
; APPLICANT: Juhlin, Claes  
; APPLICANT: Rask, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjalms, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; TITLE OF INVENTION: Thereof and DNA Encoding Same  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Martin Savitzky  
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;  
; STREET: 3C43,  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: Compaq PC  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 7.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/476,515A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:



; APPLICATION NUMBER: WO PCT/SE94/00483  
 ; FILING DATE: 24-MAY-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: SE 9301764-8  
 ; FILING DATE: 24-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Savitzky, Martin  
 ; REGISTRATION NUMBER: 29,699  
 ; REFERENCE/DOCKET NUMBER: A1355D  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-454-3816  
 ; TELEFAX: 610-454-3808  
 ; INFORMATION FOR SEQ ID NO: 69:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; FRAGMENT TYPE: internal  
 US-08-476-515A-69

Query Match 52.1%; Score 25; DB 3; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVPL 7  
 | |||:  
 Db 4 EEYVPM 9

RESULT 21  
 US-09-280-598-12  
 ; Sequence 12, Application US/09280598  
 ; Patent No. 6391584  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlessinger, Joseph  
 ; APPLICANT: Skolnik, Edward Y.  
 ; APPLICANT: Margolis, Benjamin L.  
 ; APPLICANT: App, Harold  
 ; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR  
 ; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE  
 ; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/280,598
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,820
; FILING DATE: 02-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /label= A
; OTHER INFORMATION: /note= "The tyrosine is phosphorylated."
US-09-280-598-12

```

```

Query Match          52.1%; Score 25; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches      4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 ESYVPL 7
        | |||:
Db      4 EEYVPM 9

```

# RESULT 22

US-08-602-999A-379

```

; Sequence 379, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

```

; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-379

```

```

Query Match          52.1%; Score 25; DB 3; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches    4; Conservative    1; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          5 VPLFP 9
             :||||
Db          7 LPLFP 11

```

```

RESULT 23
US-09-500-124-379
; Sequence 379, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```

```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-379

```

```

Query Match          52.1%; Score 25; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches      4; Conservative 1; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 VPLFP 9
        :||||
Db      7 LPLFP 11

```

```

RESULT 24
US-08-213-419B-7
; Sequence 7, Application US/08213419B
; Patent No. 6333406
; GENERAL INFORMATION:
; APPLICANT: Inselburg, J. et al.
; TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: JII-002CNCP
; CURRENT APPLICATION NUMBER: US/08/213,419B
; CURRENT FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: US 07/870,506
; PRIOR FILING DATE: 1992-04-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Plasmodium falciparum

```

US-08-213-419B-7

Query Match 52.1%; Score 25; DB 4; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VESYVPLF 8  
::||: ||  
Db 1 MKSYISLF 8

RESULT 25

US-09-060-299-403

; Sequence 403, Application US/09060299  
; Patent No. 6545137

; GENERAL INFORMATION:

; APPLICANT: Todd, John A  
; APPLICANT: Hess, John W  
; APPLICANT: Caskey, Charles T  
; APPLICANT: Cox, Roger D  
; APPLICANT: Gerhold, David  
; APPLICANT: Hammond, Holly  
; APPLICANT: Hey, Patricia  
; APPLICANT: Kawaguchi, Yoshihiko  
; APPLICANT: Merriman, Tony R  
; APPLICANT: Metzker, Michael L  
; TITLE OF INVENTION: No. 6545137el Receptor  
; NUMBER OF SEQUENCES: 455

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon and Vanderhye  
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: US

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/060,299  
; FILING DATE: 15-APR-1998  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/043,553  
; FILING DATE: 15-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/048,740  
; FILING DATE: 05-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: B.J.Sadoff  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 620-35

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4091  
; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 403:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-060-299-403

Query Match 52.1%; Score 25; DB 4; Length 17;  
Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
|| |||  
Db 1 SYFHLFP 7

RESULT 26

US-09-402-923A-403

; Sequence 403, Application US/09402923A  
; Patent No. 6555654

; GENERAL INFORMATION:

; APPLICANT: Todd, John A  
; Hess, John W  
; Caskey, Charles T  
; Cox, Roger D  
; Gerhold, David  
; Hammond, Holly  
; Hey, Patricia  
; Kawaguchi, Yoshihiko  
; Merriman, Tony R  
; Metzker, Michael L

; TITLE OF INVENTION: No. 6555654e1 LDL-Receptor

; NUMBER OF SEQUENCES: 455

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon and Vanderhye  
; STREET: 1100 No. 6555654th Glebe Road, Eighth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: VA 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/402,923A  
; FILING DATE: 14-Feb-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB98/01102  
; FILING DATE: 15-APR-1998  
; APPLICATION NUMBER: US 60/043,553  
; FILING DATE: 15-APR-1997  
; APPLICATION NUMBER: US 60/048,740  
; FILING DATE: 05-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: B.J.Sadoff  
; REGISTRATION NUMBER: 36,663

; REFERENCE/DOCKET NUMBER: 620-81  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4091  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 403:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:  
US-09-402-923A-403

Query Match 52.1%; Score 25; DB 4; Length 17;  
Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYVPLFP 9  
|| |||  
Db 1 SYFHLFP 7

RESULT 27  
US-08-837-593-13  
; Sequence 13, Application US/08837593  
; Patent No. 5977442  
; GENERAL INFORMATION:  
; APPLICANT: Klessig, Daniel F.  
; APPLICANT: Zhang Zhuqun  
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced  
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance  
in Plants  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
; ADDRESSEE: P.C.  
; STREET: 1601 Market Street, Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,593  
; FILING DATE: April 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029,805  
; FILING DATE: October 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:

US-08-837-593-13

Query Match 50.0%; Score 24; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||||  
Db 2 PLFP 5

RESULT 28

US-09-266-764-16

; Sequence 16, Application US/09266764  
; Patent No. 6545139  
; GENERAL INFORMATION:  
; APPLICANT: Baylor College of Medicine  
; TITLE OF INVENTION: Compositions and Methods For the Treatment and  
; TITLE OF INVENTION: Prevention of Metastatic Disorders  
; FILE REFERENCE: 00A146.0122  
; CURRENT APPLICATION NUMBER: US/09/266,764  
; CURRENT FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/077,934  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus sp.

US-09-266-764-16

Query Match 50.0%; Score 24; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||||  
Db 6 PLFP 9

RESULT 29

US-08-066-299-3



```

; Sequence 3, Application US/08066299
; Patent No. 5445947
; GENERAL INFORMATION:
;   APPLICANT: James George Metz
;   APPLICANT: Kathryn Dennis Lardizabal
;   APPLICANT: Michael W. Lassner
;   TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
;   TITLE OF INVENTION: O-Acyltransferases
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Calgene, Inc.
;     STREET: 1920 Fifth Street
;     CITY: Davis
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 95616
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
;     COMPUTER: Apple Macintosh
;     OPERATING SYSTEM: Macintosh 6.0.7
;     SOFTWARE: Microsoft Word 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/066,299
;     FILING DATE: 19930520
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/796,256
;     FILING DATE: 20-NOVEMBER-1991
;     APPLICATION NUMBER: 07/933,411
;     FILING DATE: 21-AUGUST-1992
;     APPLICATION NUMBER: PCT/US92/09863
;     FILING DATE: 13-NOVEMBER-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Elizabeth Lassen
;     REGISTRATION NUMBER: 31,845
;     NAME: Donna E. Scherer
;     REGISTRATION NUMBER: 34,719
;     REFERENCE/DOCKET NUMBER: CGNE 98
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (916) 753-6313
;     TELEFAX: (916) 753-1510
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-066-299-3

```

```

Query Match          50.0%; Score 24; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches      4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 ESYVP 6
        |:|
Db      1 ETYVP 5

```

RESULT 30

US-08-362-232-3

; Sequence 3, Application US/08362232

; Patent No. 5641667

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Fructosyltransferase Enzyme, Method

; TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann & Baron

; STREET: 350 Jericho Turnpike

; CITY: Jericho

; STATE: New York

; COUNTRY: United States of America

; ZIP: 11758

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 6.0 for DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/362,232

; FILING DATE: 22-December-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: CU 125/93

; FILING DATE: 23-December-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Baron, Ronald J.

; REGISTRATION NUMBER: 29,281

; REFERENCE/DOCKET NUMBER: 294-29

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 822-3550

; TELEFAX: (516) 822-3582

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-08-362-232-3

Query Match 50.0%; Score 24; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9

||||

Db 3 PLFP 6

RESULT 31

US-08-265-047-7

; Sequence 7, Application US/08265047

; Patent No. 5679881  
; GENERAL INFORMATION:  
; APPLICANT: Metz, James G.  
; APPLICANT: Lardizabal, Kathryn D.  
; APPLICANT: Lassner, Michael  
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic  
Protein Inv  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calgene, Inc.  
; STREET: 1920 Fifth Street  
; CITY: Davis  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 95616  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.0  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/265,047  
; FILING DATE: 23-JUN-94  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/160,602  
; FILING DATE: 30-NOV-93  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/796,256  
; FILING DATE: 20-NOV-91  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/933,411  
; FILING DATE: 21-AUG-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/066,299  
; FILING DATE: 20-MAY-93  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09863  
; FILING DATE: 13-NOV-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth Lassen  
; REGISTRATION NUMBER: 31,845  
; NAME: Donna E. Scherer  
; REGISTRATION NUMBER: 34,719  
; NAME: Carl J. Schwedler  
; REGISTRATION NUMBER: 36,924  
; REFERENCE/DOCKET NUMBER: CGNE 101-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (916) 753-6313  
; TELEFAX: (916) 753-1510  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 residues  
; TYPE: amino acids  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-265-047-7

Query Match 50.0%; Score 24; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVP 6  
|:| |  
Db 1 ETYVP 5

RESULT 32

US-08-814-196-3

; Sequence 3, Application US/08814196  
; Patent No. 5731173

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Fructosyltransferase Enzyme, Method  
; TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann & Baron  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11758

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.0 for DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/814,196  
; FILING DATE: 10-MAR-1997  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/362,232  
; FILING DATE: 22-December-1994  
; APPLICATION NUMBER: CU 125/93  
; FILING DATE: 23-December-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Baron, Ronald J.  
; REGISTRATION NUMBER: 29,281  
; REFERENCE/DOCKET NUMBER: 294-29

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO

US-08-814-196-3

Query Match 50.0%; Score 24; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||||  
Db 3 PLFP 6

RESULT 33

US-08-630-645-10

; Sequence 10, Application US/08630645

; Patent No. 5948763

; GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

ASSOCIATED

; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

DEPOSITS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,645

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA=1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-630-645-10

Query Match 50.0%; Score 24; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|:| :|  
Db 3 YLPYYP 8

RESULT 34

US-08-766-596A-10

; Sequence 10, Application US/08766596A

; Patent No. 6462171

; GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

; TITLE OF INVENTION: DEPOSITS

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,596A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-766-596A-10

Query Match 50.0%; Score 24; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|:| :|  
Db 3 YLPYYP 8

RESULT 35

PCT-US96-10220-10

; Sequence 10, Application PC/TUS9610220

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

ASSOCIATED

; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
DEPOSITS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10220

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US96-10220-10

Query Match 50.0%; Score 24; DB 5; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|:| :|  
Db 3 YLPYYP 8

RESULT 36

US-08-066-299-1

; Sequence 1, Application US/08066299  
; Patent No. 5445947

; GENERAL INFORMATION:

; APPLICANT: James George Metz  
; APPLICANT: Kathryn Dennis Lardizabal  
; APPLICANT: Michael W. Lassner  
; TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol  
; TITLE OF INVENTION: O-Acyltransferases  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calgene, Inc.  
; STREET: 1920 Fifth Street  
; CITY: Davis  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 95616

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.7  
; SOFTWARE: Microsoft Word 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/066,299  
; FILING DATE: 19930520  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/796,256  
; FILING DATE: 20-NOVEMBER-1991  
; APPLICATION NUMBER: 07/933,411  
; FILING DATE: 21-AUGUST-1992  
; APPLICATION NUMBER: PCT/US92/09863  
; FILING DATE: 13-NOVEMBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Elizabeth Lassen  
; REGISTRATION NUMBER: 31,845  
; NAME: Donna E. Scherer  
; REGISTRATION NUMBER: 34,719  
; REFERENCE/DOCKET NUMBER: CGNE 98

; TELECOMMUNICATION INFORMATION:



; TELEPHONE: (916) 753-6313  
; TELEFAX: (916) 753-1510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-066-299-1

Query Match 50.0%; Score 24; DB 1; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVP 6  
|:| | |  
Db 1 ETYVP 5

RESULT 37

US-08-128-971B-6

; Sequence 6, Application US/08128971B  
; Patent No. 5525503  
; GENERAL INFORMATION:  
; APPLICANT: Christopher E. Rudd  
; APPLICANT: Prasad Kanteti  
; TITLE OF INVENTION: SIGNAL TRANSDUCTION VIA CD28  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/128,971B  
; FILING DATE: September 28, 1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janis K. Fraser  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00530/073001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-128-971B-6

Query Match 50.0%; Score 24; DB 1; Length 11;  
Best Local Similarity 37.5%; Pred. No. 2.3e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
: |:|: |  
Db 2 DGYMPMSP 9

RESULT 38

US-08-265-047-5

; Sequence 5, Application US/08265047

; Patent No. 5679881

; GENERAL INFORMATION:

; APPLICANT: Metz, James G.

; APPLICANT: Lardizabal, Kathryn D.

; APPLICANT: Lassner, Michael

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protein Inv

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Calgene, Inc.

; STREET: 1920 Fifth Street

; CITY: Davis

; STATE: CA

; COUNTRY: USA

; ZIP: 95616

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.0

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/265,047

; FILING DATE: 23-JUN-94

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/160,602

; FILING DATE: 30-NOV-93

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/796,256

; FILING DATE: 20-NOV-91

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/933,411

; FILING DATE: 21-AUG-92

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/066,299

; FILING DATE: 20-MAY-93

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/09863

```

; FILING DATE: 13-NOV-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 101-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 residues
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-265-047-5

```

```

Query Match          50.0%; Score 24; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches      4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 ESYVP 6
        |:|
Db      1 ETYVP 5

```

# RESULT 39

US-08-652-877-50

```

; Sequence 50, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-652-877-50

```

```

Query Match          50.0%; Score 24; DB 3; Length 11;
Best Local Similarity 37.5%; Pred. No. 2.3e+02;
Matches      3; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      2 ESYVPLFP 9
        : |:|: |
Db      4 DGYMPMSP 11

```

#### RESULT 40

```

US-08-476-515A-50
; Sequence 50, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;

```

```

; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-515A-50

```

```

Query Match          50.0%;  Score 24;  DB 3;  Length 11;
Best Local Similarity 37.5%;  Pred. No. 2.3e+02;
Matches      3;  Conservative      3;  Mismatches      2;  Indels      0;  Gaps      0;

```

```

Qy      2 ESYVPLFP 9
        : |:|: |
Db      4 DGYMPMSP 11

```

# RESULT 41

US-08-318-794-1

; Sequence 1, Application US/08318794

; Patent No. 6022726

; GENERAL INFORMATION:

; APPLICANT: Palese, Peter

; TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED

```

; TITLE OF INVENTION:  VIRUSES
; NUMBER OF SEQUENCES:  36
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/318,794
;   FILING DATE:  20-DEC-1994
;   CLASSIFICATION:  424
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Coruzzi, Laura A.
;   REGISTRATION NUMBER:  30,742
;   REFERENCE/DOCKET NUMBER:  7682-019
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  12 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-08-318-794-1

```

```

Query Match          50.0%;  Score 24;  DB 3;  Length 12;
Best Local Similarity 80.0%;  Pred. No. 2.5e+02;
Matches      4;  Conservative    1;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      2 ESYVP 6
        :||||
Db      3 DSYVP 7

```

# RESULT 42

US-08-470-106-1

```

; Sequence 1, Application US/08470106
; Patent No. 6316243
; GENERAL INFORMATION:
;   APPLICANT:  Palese, Peter
;   TITLE OF INVENTION:  GENETICALLY ENGINEERED ATTENUATED
;                       VIRUSES
;   NUMBER OF SEQUENCES:  36
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Pennie & Edmonds
;     STREET:  1155 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York

```

```

;          COUNTRY: U.S.A.
;          ZIP: 10036-2711
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/08/470,106
;          FILING DATE: 06-Jun-1995
;          CLASSIFICATION: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Coruzzi, Laura A.
;          REGISTRATION NUMBER: 30,742
;          REFERENCE/DOCKET NUMBER: 7682-025
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 790-9090
;          TELEFAX: (212) 869-9741/8864
;          TELEX: 66141 PENNIE
;    INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 12 amino acids
;            TYPE: amino acid
;            TOPOLOGY: unknown
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-470-106-1

```

```

Query Match          50.0%;  Score 24;  DB 4;  Length 12;
Best Local Similarity 80.0%;  Pred. No. 2.5e+02;
Matches      4;  Conservative    1;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          2 ESYVP 6
            :||||
Db          3 DSYVP 7

```

#### RESULT 43

```

US-08-408-604A-37
; Sequence 37, Application US/08408604A
; Patent No. 5801149
;    GENERAL INFORMATION:
;    APPLICANT: Shoelson, Steven
;    TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
;    NUMBER OF SEQUENCES: 211
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: LAHIVE & COCKFIELD
;      STREET: 60 State Street, Suite 510
;      CITY: Boston
;      STATE: Massachusetts
;      COUNTRY: USA
;      ZIP: 02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,604A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/134,558
; FILING DATE: 08-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,949
; FILING DATE: 09-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/722,359
; FILING DATE: 19-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-014CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-408-604A-37

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Query Match          50.0%; Score 24; DB 1; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.7e+02;
Matches      3; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      2 ESYVPLFP 9
        : |:|: |
Db      3 DGYMPMSP 10

```

#### RESULT 44

PCT-US93-09626-37

; Sequence 37, Application PC/TUS9309626

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES

; NUMBER OF SEQUENCES: 48

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII (text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/09626

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/959,949

; FILING DATE: October 9, 1992

; APPLICATION NUMBER: 07/722,359

; FILING DATE: June 19, 1991

; INFORMATION FOR SEQ ID NO: 37:



; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US93-09626-37

Query Match 50.0%; Score 24; DB 5; Length 13;  
Best Local Similarity 37.5%; Pred. No. 2.7e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
: |:|: |  
Db 3 DGYMPMSP 10

RESULT 45

US-08-103-490A-23

; Sequence 23, Application US/08103490A  
; Patent No. 5422341  
; GENERAL INFORMATION:  
; APPLICANT: Macielag, Mark J.  
; TITLE OF INVENTION: Motilin-Like Polypeptides With  
; TITLE OF INVENTION: Gastrointestinal Motor Stimulating Activity  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The BOC Group, Inc.  
; STREET: 100 Mountain Avenue  
; CITY: Murray Hill  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07974  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/103,490A  
; FILING DATE: 06-AUG-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swope, R. Hain  
; REGISTRATION NUMBER: 24,864  
; REFERENCE/DOCKET NUMBER: 92H817  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-771-6292  
; TELEFAX: 908-771-6159  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-103-490A-23

Query Match 50.0%; Score 24; DB 1; Length 14;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPLF 8  
:||||  
Db 1 FVPLF 5

RESULT 46

US-08-103-490A-40

; Sequence 40, Application US/08103490A

; Patent No. 5422341

; GENERAL INFORMATION:

; APPLICANT: Macielag, Mark J.

; TITLE OF INVENTION: Motilin-Like Polypeptides With

; TITLE OF INVENTION: Gastrointestinal Motor Stimulating Activity

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The BOC Group, Inc.

; STREET: 100 Mountain Avenue

; CITY: Murray Hill

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07974

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/103,490A

; FILING DATE: 06-AUG-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Swope, R. Hain

; REGISTRATION NUMBER: 24,864

; REFERENCE/DOCKET NUMBER: 92H817

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-771-6292

; TELEFAX: 908-771-6159

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-103-490A-40

Query Match 50.0%; Score 24; DB 1; Length 14;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPLF 8  
:||||  
Db 1 FVPLF 5

RESULT 47

US-08-602-999A-319

; Sequence 319, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 319:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-602-999A-319

Query Match 50.0%; Score 24; DB 3; Length 15;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9

: |||: |

Db 2 DEYVPVPP 9

RESULT 48

US-08-743-168B-26

```
; Sequence 26, Application US/08743168B
; Patent No. 6271015
; GENERAL INFORMATION:
;   APPLICANT: Gilula, No. 6271015ton B
;   APPLICANT: Cravatt, Benjamin F
;   APPLICANT: Lerner, Richard A
;   TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
;   NUMBER OF SEQUENCES: 54
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: The Scripps Research Institute
;     STREET: 10550 No. 6271015th Torrey Pines Road
;     CITY: La Jolla
;     STATE: California
;     COUNTRY: US
;     ZIP: 92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/743,168B
;     FILING DATE: 04-NOV-1996
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/489,535
;     FILING DATE: 12-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fitting, Thomas
;     REGISTRATION NUMBER: 34,163
;     REFERENCE/DOCKET NUMBER: TSRI 485.2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 784-2937
;     TELEFAX: (619) 784-9399
;   INFORMATION FOR SEQ ID NO: 26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FRAGMENT TYPE: internal
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US-08-743-168B-26

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Query Match          50.0%; Score 24; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          6 PLFP 9
            ||||
Db          12 PLFP 15
```

RESULT 49

US-08-743-168B-27

```

; Sequence 27, Application US/08743168B
; Patent No. 6271015
; GENERAL INFORMATION:
;   APPLICANT:  Gilula, No. 6271015ton B
;   APPLICANT:  Cravatt, Benjamin F
;   APPLICANT:  Lerner, Richard A
;   TITLE OF INVENTION:  FATTY-ACID AMIDE HYDROLASE
;   NUMBER OF SEQUENCES:  54
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  The Scripps Research Institute
;     STREET:    10550 No. 6271015th Torrey Pines Road
;     CITY:      La Jolla
;     STATE:     California
;     COUNTRY:   US
;     ZIP:       92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/743,168B
;     FILING DATE:       04-NOV-1996
;     CLASSIFICATION:    435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/489,535
;     FILING DATE:       12-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fitting, Thomas
;     REGISTRATION NUMBER:  34,163
;     REFERENCE/DOCKET NUMBER:  TSRI 485.2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (619) 784-2937
;     TELEFAX:   (619) 784-9399
;   INFORMATION FOR SEQ ID NO: 27:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:    amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-08-743-168B-27

```

```

Query Match          50.0%;  Score 24;  DB 3;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 3.1e+02;
Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          6 PLFP 9
            ||||
Db          2 PLFP 5

```

```

RESULT 50
US-09-500-124-319
; Sequence 319, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:

```

```

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 319:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-319

```

```

Query Match          50.0%; Score 24; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches    4; Conservative    2; Mismatches    2; Indels    0; Gaps    0;

```

```

Qy      2 ESYVPLFP 9
        : |||: |
Db      2 DEYVPVPP 9

```

```

Search completed: July  4, 2004, 04:48:52
Job time : 6.64179 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 6.91791 Seconds  
(without alignments)  
125.142 Million cell updates/sec

Title: US-09-641-802-31  
Perfect score: 48  
Sequence: 1 VESYVPLFP 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	25	52.1	11	2	I33098	173K exoantigen -
2	25	52.1	18	2	S36121	lectin - spurge (E
3	23	47.9	15	2	B41868	hypothetical prote
4	23	47.9	18	2	A54651	insulin-like growt
5	21	43.8	11	2	I60434	68kDa neurofilamen
6	21	43.8	12	2	A61503	sterol carrier pro
7	21	43.8	14	2	D61308	hemocyanin chain 5
8	21	43.8	15	2	B59045	alpha-conotoxin Au
9	21	43.8	15	2	S29485	GTP-binding protei
10	21	43.8	16	2	C59045	alpha-conotoxin Au
11	21	43.8	16	2	A59045	alpha-conotoxin Au
12	21	43.8	18	2	S56715	hydroxymethylgluta
13	20	41.7	10	2	D28027	protein P7 - curle

14	20	41.7	11	2	PN0042	stathmin - mouse (
15	20	41.7	14	2	A61308	hemocyanin chain 2
16	20	41.7	15	2	B59137	protein Pf1 - gold
17	20	41.7	18	2	A28027	protein P2 - curle
18	20	41.7	18	2	B35910	neurofibromatosis-
19	19	39.6	13	2	S01119	photosystem II pro
20	19	39.6	13	2	S21152	tryptophyllin-rela
21	19	39.6	13	2	A05174	tryptophyllin-13 -
22	19	39.6	14	2	S22236	lipxygenase (EC 1
23	19	39.6	15	2	S77988	cytochrome-c oxida
24	19	39.6	16	2	B36300	T-cell receptor de
25	19	39.6	17	2	S59481	hydroxyproline-ric
26	19	39.6	18	2	S09731	photosystem I prot
27	18.5	38.5	14	2	PL0152	metal-binding prot
28	18	37.5	9	2	A60356	118K stomach cance
29	18	37.5	11	2	S78026	ribosomal protein
30	18	37.5	12	2	S01122	photosystem II 3.7
31	18	37.5	12	2	S74196	3-hydroxy-3-methyl
32	18	37.5	13	2	A59387	VCAM-1 5'UTR bindi
33	18	37.5	13	2	PH0805	T-cell receptor al
34	18	37.5	13	2	I77387	AMP deaminase - ra
35	18	37.5	13	2	PC4391	cysteine proteinas
36	18	37.5	14	2	PH1566	cerebrin 30 - huma
37	18	37.5	14	2	PN0666	dystrophin-associa
38	18	37.5	14	2	C59137	protein Pf3 - gold
39	18	37.5	15	1	LFECF	phe operon leader
40	18	37.5	15	2	PW0004	chlorophyll a/b-bi
41	18	37.5	15	2	PN0665	dystrophin-associa
42	18	37.5	16	2	T09741	photosystem I chai
43	18	37.5	16	2	S38292	30K allergen - rye
44	18	37.5	17	2	S17274	ribosomal protein
45	18	37.5	18	2	I52614	u-plasminogen acti
46	18	37.5	18	2	JP0102	fibrinogen beta ch
47	17	35.4	11	2	A57458	gene Gax protein -
48	17	35.4	11	2	A58838	hemolysin - Porphy
49	17	35.4	12	2	JU0356	cycloleonorinin -
50	17	35.4	13	2	S78766	ribosomal protein
51	17	35.4	13	2	PH0756	T-cell receptor be
52	17	35.4	14	2	S29209	avenin alpha-2 - o
53	17	35.4	14	2	B36079	hypothetical prote
54	17	35.4	14	2	B20872	alpha-2-macroglobu
55	17	35.4	14	2	PH1614	Ig H chain V-D-J r
56	17	35.4	15	2	S29207	avenin gamma-4 - o
57	17	35.4	15	2	PS0455	superoxide dismuta
58	17	35.4	15	2	PA0055	protein QF200007 -
59	17	35.4	15	2	PH0772	T-cell receptor be
60	17	35.4	16	2	C61414	chymotrypsin (EC 3
61	17	35.4	16	2	PH0749	T-cell receptor be
62	17	35.4	16	2	B40291	cytochrome P450mtf
63	17	35.4	17	2	B31435	adherence lectin 1
64	17	35.4	17	2	A61557	major merozoite su
65	17	35.4	17	2	S60171	sex-lethal protein
66	17	35.4	17	2	B61414	chymotrypsin (EC 3
67	17	35.4	17	2	PH1312	Ig heavy chain DJ
68	17	35.4	18	2	S57518	T cell receptor be
69	16	33.3	7	2	A61081	tryptophyllin, bas
70	16	33.3	9	2	S66419	tetrameric protein



71	16	33.3	9	2	PT0324	Ig heavy chain CRD
72	16	33.3	10	2	S23307	neurokinin A - rai
73	16	33.3	10	2	S23186	neurokinin A - Atl
74	16	33.3	11	2	D61033	ranatachykinin D -
75	16	33.3	11	2	S04875	nifS protein - Bra
76	16	33.3	11	2	A26120	6-phosphofructokin
77	16	33.3	13	2	A60458	protocatechuate 3,
78	16	33.3	13	2	B26093	microbial collagen
79	16	33.3	13	2	S47388	T-cell antigen rec
80	16	33.3	14	2	S38307	DEB-A protein - fr
81	16	33.3	14	2	S00150	ovostatin - duck (
82	16	33.3	14	2	PH1806	T cell receptor al
83	16	33.3	15	2	S20410	protein kinase (EC
84	16	33.3	15	2	PA0027	protein QA100006 -
85	16	33.3	15	2	A36279	chemoattractant pr
86	16	33.3	15	2	A41436	alpha-macroglobuli
87	16	33.3	15	2	B41436	ovostatin - green
88	16	33.3	16	2	S21184	hemocyte proteinas
89	16	33.3	16	2	A20190	hypodermin B - ear
90	16	33.3	16	2	A42411	myosin light chain
91	16	33.3	16	2	A45454	ankyrin-binding gl
92	16	33.3	16	4	A33171	hypothetical prote
93	16	33.3	17	2	S57519	T cell receptor be
94	16	33.3	17	2	S57556	T cell receptor be
95	16	33.3	17	2	A35550	adrenocortical cel
96	16	33.3	18	2	B49215	urease (EC 3.5.1.5
97	15.5	32.3	18	2	S40502	20-alpha-hydroxyst
98	15	31.2	8	2	G33098	205K exoantigen -
99	15	31.2	8	2	S10783	enamelin f - bovin
100	15	31.2	8	4	I54017	granulocyte-colony

#### ALIGNMENTS

##### RESULT 1

I33098

173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: I33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: I33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIC>

Query Match 52.1%; Score 25; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 97;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLFP 9

:||||

Db 6 LPLFP 10

RESULT 2

S36121

lectin - spurge (*Euphorbia characias*)

C;Species: *Euphorbia characias*

C;Date: 09-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997

C;Accession: S36121

R;Stirpe, F.; Licastro, F.; Morini, M.C.; Parente, A.; Savino, G.; Abbondanza, A.; Bolognesi, A.; Falasca, A.I.; Rossi, C.A.

Biochim. Biophys. Acta 1158, 33-39, 1993

A;Title: Purification and partial characterization of a mitogenic lectin from the latex of *Euphorbia marginata*.

A;Reference number: S36120; MUID:93357266; PMID:8353129

A;Accession: S36121

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <SNI>

Query Match 52.1%; Score 25; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVPL 7

||| |:

Db 2 ESYTPI 7

RESULT 3

B41868

hypothetical protein (traE1 3' region) - *Enterococcus faecalis* plasmid pAD1

C;Species: *Enterococcus faecalis*

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Oct-1999

C;Accession: B41868; B37391

R;Pontius, L.T.; Clewell, D.B.

J. Bacteriol. 174, 3152-3160, 1992

A;Title: Conjugative transfer of *Enterococcus faecalis* plasmid pAD1: nucleotide sequence and transcriptional fusion analysis of a region involved in positive regulation.

A;Reference number: A41868; MUID:92250408; PMID:1315730

A;Contents: plasmid pAD1

A;Accession: B41868

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-15 <PON>

A;Note: sequence extracted from NCBI backbone (NCBIN:99901, NCBIP:99906)

R;Clewell, D.B.; Pontius, L.T.; An, F.Y.; Ike, Y.; Suzuki, A.; Nakayama, J.  
Plasmid 24, 156-161, 1990

A;Title: Nucleotide sequence of the sex pheromone inhibitor (iAD1) determinant of *Enterococcus faecalis* conjugative plasmid pAD1.

A;Reference number: A37391; MUID:91261999; PMID:2128961

A;Accession: B37391

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-15 <CLE>

A;Cross-references: GB:M62888; NID:g141853; PIDN:AAA98040.1; PID:g141855

C;Genetics:

A;Genome: plasmid

Query Match 47.9%; Score 23; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLF 8  
| 1:| |  
Db 4 VHVYIPRF 11

#### RESULT 4

A54651

insulin-like growth factor-binding protein 22K form - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 11-Apr-1995

C;Accession: A54651

R;Roghani, M.; Segovia, B.; Whitechurch, O.; Binoux, M.

Growth Regul. 1, 125-130, 1991

A;Title: Purification from human cerebrospinal fluid of insulin-like growth factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form of IGFBP-3 and a new IGFBP species.

A;Reference number: A54651; MUID:93091816; PMID:1726837

A;Accession: A54651

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <ROG>

A;Experimental source: cerebrospinal fluid

A;Note: sequence extracted from NCBI backbone (NCBIP:121074)

Query Match 47.9%; Score 23; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
:|:| |  
Db 1 DSFVPXEP 8

#### RESULT 5

I60434

68kDa neurofilament - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I60434

R;Reeben, M.; Neuman, T.; Palgi, J.; Palm, K.; Paalme, V.; Saarma, M.

J. Neurosci. Res. 40, 177-188, 1995

A;Title: Characterization of the rat light neurofilament (NF-L) gene promoter and identification of NGF and cAMP responsive regions.

A;Reference number: I60434; MUID:95264348; PMID:7745611

A;Accession: I60434

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: EMBL:X53981; NID:g452676; PIDN:CAA37931.1; PID:g452677

C;Genetics:

A;Gene: NF68

Query Match 43.8%; Score 21; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8  
|||  
Db 5 SYEPYF 10

RESULT 6

A61503

sterol carrier protein-2-like protein - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 11-May-2000

C;Accession: A61503

R;Reinhart, M.P.; Avart, S.J.; Foglia, T.

Comp. Biochem. Physiol. B 100, 243-248, 1991

A;Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken SCP-2-like protein.

A;Reference number: A61503; MUID:92191564; PMID:1799965

A;Accession: A61503

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <REI>

Query Match 43.8%; Score 21; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 6.4e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|||  
Db 3 PLYP 6

RESULT 7

D61308

hemocyanin chain 5A - Sahara scorpion (fragment)

C;Species: Androctonus australis (Sahara scorpion)

C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999

C;Accession: D61308

R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in Androctonus australis haemocyanin.

A;Reference number: A61308; MUID:80047238; PMID:499512

A;Accession: D61308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <JOL>

Query Match 43.8%; Score 21; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 7.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLF 8  
| :|||  
Db 7 ERLLPLF 13

RESULT 8

B59045

alpha-conotoxin AuIB - cone shell (Conus aulicus)

C;Species: Conus aulicus (court cone)

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999

C;Accession: B59045

R;Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McIntosh, J.M.

J. Neurosci. 18, 8571-8579, 1998

A;Title: Alpha-conotoxin AuIB selectively blocks alpha3beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release.

A;Reference number: A59045; MUID:99003392; PMID:9786965

A;Accession: B59045

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <LUO>

C;Superfamily: alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin; venom

F;1-15/Product: alpha-conotoxin AuIB #status experimental <MAT>

F;2-8,3-15/Disulfide bonds: #status experimental

F;15/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 43.8%; Score 21; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8

|| ||

Db 4 SYPPCF 9

RESULT 9

S29485

GTP-binding protein o-ral - Pacific electric ray (fragment)

C;Species: Torpedo californica (Pacific electric ray)

C;Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997

C;Accession: S29485

R;Volkmandt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.

FEBS Lett. 317, 53-56, 1993

A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicles.

A;Reference number: S29485; MUID:93154521; PMID:8428634

A;Accession: S29485

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <VOL>

Query Match 43.8%; Score 21; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVP 6

|| ||

Db 6 VEDYEP 11

RESULT 10

C59045

alpha-conotoxin AuIC - cone shell (Conus aulicus)

C;Species: Conus aulicus (court cone)

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999

C;Accession: C59045

R;Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McIntosh, J.M.

J. Neurosci. 18, 8571-8579, 1998

A;Title: Alpha-conotoxin AuIB selectively blocks alpha3beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release.

A;Reference number: A59045; MUID:99003392; PMID:9786965

A;Accession: C59045

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <LUO>

C;Superfamily: alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin; venom

F;1-16/Product: alpha-conotoxin AuIC #status experimental <MAT>

F;2-8,3-16/Disulfide bonds: #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 43.8%; Score 21; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 8.7e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8

|| ||

Db 4 SYPPCF 9

RESULT 11

A59045

alpha-conotoxin AuIA - cone shell (Conus aulicus)

C;Species: Conus aulicus (court cone)

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999

C;Accession: A59045

R;Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McIntosh, J.M.

J. Neurosci. 18, 8571-8579, 1998

A;Title: Alpha-conotoxin AuIB selectively blocks alpha3beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release.

A;Reference number: A59045; MUID:99003392; PMID:9786965

A;Accession: A59045

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <LUO>

C;Superfamily: alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin; venom

F;1-16/Product: alpha-conotoxin AuIA #status experimental <MAT>

F;2-8,3-16/Disulfide bonds: #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 43.8%; Score 21; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8  
|||  
Db 4 SYPPCF 9

RESULT 12

S56715

hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) (clone hmg3.2) -  
potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 03-Jun-2002

C;Accession: S56715

R;Bhattacharyya, M.K.; Paiva, N.L.; Dixon, R.A.; Korth, K.L.; Stermer, B.A.  
Plant Mol. Biol. 28, 1-15, 1995

A;Title: Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase in  
potato.

A;Reference number: S56710; MUID:95306778; PMID:7787174

A;Accession: S56715

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-18 <BHA>

A;Cross-references: EMBL:L34830; NID:g529524; PIDN:AAC37437.1; PID:g553101

C;Superfamily: hydroxymethylglutaryl-CoA reductase (NADPH)

C;Keywords: coenzyme A; oxidoreductase

Query Match 43.8%; Score 21; DB 2; Length 18;  
Best Local Similarity 75.0%; Pred. No. 9.9e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|||  
Db 10 PLYP 13

RESULT 13

D28027

protein P7 - curled-leaved tobacco (fragment)

C;Species: Nicotiana glauca (curled-leaved tobacco)

C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993

C;Accession: D28027

R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal  
amino acid-sequence analysis of proteins electroblotted from two-dimensional  
gel-separated total extracts.

A;Reference number: A94167

A;Accession: D28027

A;Molecule type: protein

A;Residues: 1-10 <BAU>

Query Match 41.7%; Score 20; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 8.4e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7  
 |:|:  
Db 5 SFVPI 9

RESULT 14

PN0042

stathmin - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C;Accession: PN0042

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0042

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 17,500 and the pI is 5.63. The amino-terminus is blocked.

C;Keywords: brain

Query Match 41.7%; Score 20; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 9.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
 || ||  
Db 3 VPDFP 7

RESULT 15

A61308

hemocyanin chain 2 - Sahara scorpion (fragment)

C;Species: Androctonus australis (Sahara scorpion)

C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999

C;Accession: A61308

R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in Androctonus australis haemocyanin.

A;Reference number: A61308; MUID:80047238; PMID:499512

A;Accession: A61308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <JOL>

Query Match 41.7%; Score 20; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLF 8  
 :| |  
Db 10 IPLF 13



RESULT 16

B59137

protein Pf1 - golden needle mushroom (fragment)

C;Species: Flammulina velutipes (golden needle mushroom)

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C;Accession: B59137

R;Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.

submitted to the Protein Sequence Database, November 1999

A;Description: Differences of proteins expressed in the fruiting dikaryon and the non-fruiting monokaryon of Flammulina velutipes.

A;Reference number: A59137

A;Accession: B59137

A;Molecule type: protein

A;Residues: 1-15 <SAK>

A;Experimental source: strain FV-4

Query Match 41.7%; Score 20; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
|||:  
Db 8 YVPM 11

RESULT 17

A28027

protein P2 - curled-leaved tobacco (fragment)

C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)

C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993

C;Accession: A28027

R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-sequence analysis of proteins electroblotted from two-dimensional gel-separated total extracts.

A;Reference number: A94167

A;Accession: A28027

A;Molecule type: protein

A;Residues: 1-18 <BAU>

A;Note: 14-Arg was also found

Query Match 41.7%; Score 20; DB 2; Length 18;  
Best Local Similarity 37.5%; Pred. No. 1.5e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
:: ||: |  
Db 6 DTIVPIAP 13

RESULT 18

B35910

neurofibromatosis-related protein NF1, long splice form - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Oct-1990 #sequence\_revision 23-Oct-1990 #text\_change 29-Aug-1997  
C;Accession: B35910  
R;Cawthon, R.M.; Weiss, R.; Xu, G.; Viskochil, D.; Culver, M.; Stevens, J.;  
Robertson, M.; Dunn, D.; Gesteland, R.; O'Connell, P.; White, R.  
Cell 62, 608b, 1990  
A;Reference number: A35910  
A;Accession: B35910  
A;Status: preliminary; nucleic acid sequence not shown; not compared with  
conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-18 <CAW>  
C;Genetics:  
A;Gene: GDB:NF1  
A;Cross-references: GDB:120231; OMIM:162200  
A;Map position: 17q11.2-17q11.2  
C;Keywords: alternative splicing; tumor suppressor

Query Match 41.7%; Score 20; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
:: |||  
Db 11 FMQLFP 16

#### RESULT 19

S01119

photosystem II protein psbK - spinach chloroplast (fragment)

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 30-Jun-1989 #sequence\_revision 31-Dec-1990 #text\_change 19-Jan-1996

C;Accession: S01119

R;Murata, N.; Miyao, M.; Hayashida, N.; Hidaka, T.; Sugiura, M.

FEBS Lett. 235, 283-288, 1988

A;Title: Identification of a new gene in the chloroplast genome encoding a low-molecular-mass polypeptide of photosystem II complex.

A;Reference number: S01119

A;Accession: S01119

A;Molecule type: protein

A;Residues: 1-13 <MUR>

C;Genetics:

A;Gene: psbK

A;Genome: chloroplast

C;Superfamily: photosystem II protein psbK

C;Keywords: chloroplast; membrane-associated complex; photosynthesis;  
photosystem II; thylakoid

Query Match 39.6%; Score 19; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
|:| | |  
Db 4 EAYAFLLXP 11

#### RESULT 20

S21152

tryptophyllin-related peptide - two-colored leaf frog

C;Species: *Phyllomedusa bicolor* (two-colored leaf frog)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S21152

R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.; Barra, D.

FEBS Lett. 302, 151-154, 1992

A;Title: Identification and characterization of two dermorphins from skin extracts of the Amazonian frog *Phyllomedusa bicolor*.

A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21152

A;Molecule type: protein

A;Residues: 1-13 <MIG>

A;Experimental source: skin

C;Superfamily: unassigned animal peptides

Query Match 39.6%; Score 19; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|::|  
Db 9 PIYP 12

RESULT 21

A05174

tryptophyllin-13 - Rohde's leaf frog

C;Species: *Phyllomedusa rohdei* (Rohde's leaf frog)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 18-Aug-2000

C;Accession: A05174

R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.

Int. J. Pept. Protein Res. 27, 175-182, 1986

A;Reference number: A05174

A;Accession: A05174

A;Molecule type: protein

A;Residues: 1-13 <MON>

C;Superfamily: unassigned animal peptides

C;Keywords: pyroglutamic acid; skin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 39.6%; Score 19; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|::|  
Db 9 PIYP 12

RESULT 22

S22236

lipoxygenase (EC 1.13.11.12) 1 - barley (fragment)

C;Species: *Hordeum vulgare* (barley)

C;Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999

C;Accession: S22236

R;Doderer, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.

Biochim. Biophys. Acta 1120, 97-104, 1992

A;Title: Purification and characterization of two lipxygenase isoenzymes from germinating barley.

A;Reference number: S21772; MUID:92207997; PMID:1554746

A;Accession: S22236

A;Molecule type: protein

A;Residues: 1-14 <DOD>

A;Experimental source: var. Triumph, seed

C;Function:

A;Description: catalyzes the peroxidation of polyunsaturates fatty acids to their corresponding hydroperoxides

C;Superfamily: lipxygenase

C;Keywords: monomer; oxidoreductase; seed

Query Match 39.6%; Score 19; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.9e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9

|: |:|

Db 3 YMLLYP 8

#### RESULT 23

S77988

cytochrome-c oxidase (EC 1.9.3.1) chain VIIa - bigeye tuna (fragment)

C;Species: Thunnus obesus (bigeye tuna)

C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 04-Sep-1998

C;Accession: S77988

R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980

A;Accession: S77988

A;Molecule type: protein

A;Residues: 1-15 <ARN>

A;Experimental source: heart; liver

C;Genetics:

A;Genome: nuclear

C;Function:

A;Pathway: oxidative phosphorylation; respiratory chain

C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain

Query Match 39.6%; Score 19; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 2e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6

:|||

Db 2 NYVP 5

#### RESULT 24

B36300

T-cell receptor delta chain V-J region - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 30-May-1997

C;Accession: B36300

R;Matis, L.A.; Fry, A.M.; Cron, R.Q.; Cotterman, M.M.; Dick, R.F.; Bluestone, J.A.

Science 245, 746-749, 1989

A;Title: Structure and specificity of a class II MHC alloreactive gammadelta T cell receptor heterodimer.

A;Reference number: A36300; MUID:89368895; PMID:2528206

A;Accession: B36300

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-16 <MAT>

C;Keywords: T-cell receptor

Query Match 39.6%; Score 19; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
|:|:  
Db 4 YIPI 7

RESULT 25

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C;Species: *Phaseolus vulgaris* (kidney bean)

C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998

C;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (*Phaseolus vulgaris* L.).

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481

A;Molecule type: protein

A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline

F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 39.6%; Score 19; DB 2; Length 17;  
Best Local Similarity 37.5%; Pred. No. 2.3e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
:|:| |  
Db 1 DMYLPPVP 8

RESULT 26

S09731

photosystem I protein psaI - spinach chloroplast (fragment)

C;Species: chloroplast *Spinacia oleracea* (spinach)

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 19-Jan-1996  
 C;Accession: S09731  
 R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.  
 FEBS Lett. 263, 274-278, 1990  
 A;Title: Polypeptide composition of higher plant photosystem I complex.  
 Identification of psaI, psaJ and psaK gene products.  
 A;Reference number: S09730; MUID:90242987; PMID:2185953  
 A;Accession: S09731  
 A;Molecule type: protein  
 A;Residues: 1-18 <IKE>  
 C;Genetics:  
 A;Gene: psaI  
 A;Genome: chloroplast  
 C;Superfamily: photosystem I protein psaI  
 C;Keywords: chloroplast; membrane-associated complex; photosynthesis;  
 photosystem I; thylakoid

Query Match 39.6%; Score 19; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

Qy 4 YVPL----FP 9  
 :||| ||  
 Db 7 FVPLVGLVFP 16

#### RESULT 27

PL0152

metal-binding protein - reticulate nassa (fragment)

C;Species: Nassarius reticulatus (reticulate nassa)

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Jun-2000

C;Accession: PL0152

R;Andersen, R.A.; Eriksen, K.D.H.; Bakke, T.

Comp. Biochem. Physiol. B 94, 285-291, 1989

A;Title: Evidence of presence of a low molecular weight, non-metallothionein-  
 like metal-binding protein in the marine gastropod Nassarius reticulatus L.

A;Reference number: PL0152

A;Accession: PL0152

A;Molecule type: protein

A;Residues: 1-14 <AND>

C;Comment: This protein is induced in environments contaminated with heavy  
 metal.

Query Match 38.5%; Score 18.5; DB 2; Length 14;  
 Best Local Similarity 71.4%; Pred. No. 2.3e+03;  
 Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 2 ESYVPLF 8  
 | | |||  
 Db 8 EXY-PLF 13

#### RESULT 28

A60356

118K stomach cancer antigen - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 17-Mar-1999

C;Accession: A60356

R;Shiraishi, Y.

Int. J. Cancer 45, 783-787, 1990

A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens from carcinogen-transformed bloom syndrome cells.

A;Reference number: A60356; MUID:90216080; PMID:2323853

A;Accession: A60356

A;Molecule type: protein

A;Residues: 1-9 <SHI>

C;Keywords: glycoprotein

Query Match 37.5%; Score 18; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9

:|||

Db 1 IPLKP 5

#### RESULT 29

S78026

ribosomal protein YmL29, mitochondrial - yeast (*Saccharomyces cerevisiae*) (fragment)

C;Species: *Saccharomyces cerevisiae*

C;Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997

C;Accession: S78026

R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittmann-Liebold, B.; Nishimura, T.; Isono, K.

Eur. J. Biochem. 245, 449-456, 1997

A;Title: Identification and characterization of the genes for mitochondrial ribosomal proteins of *Saccharomyces cerevisiae*.

A;Reference number: S78018; MUID:97296414; PMID:9151978

A;Accession: S78026

A;Molecule type: protein

A;Residues: 1-11 <KIT>

C;Genetics:

A;Genome: nuclear

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 37.5%; Score 18; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

Qy 2 ESYVPLFP 9

|:|: ||

Db 3 EAYI--FP 8

#### RESULT 30

S01122

photosystem II 3.7K protein - spinach (fragment)

C;Species: *Spinacia oleracea* (spinach)

C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993

C;Accession: S01122

R;Schroeder, W.P.; Henrysson, T.; Akerlund, H.E.

FEBS Lett. 235, 289-292, 1988

A;Title: Characterization of low molecular mass proteins of photosystem II by N-terminal sequencing.

A;Reference number: S01120

A;Accession: S01122

A;Molecule type: protein

A;Residues: 1-12 <SCH>

C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 37.5%; Score 18; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
|:| | |  
Db 4 EAYAFLLSP 11

#### RESULT 31

S74196

3-hydroxy-3-methylglutaryl CoA synthase homolog - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 01-May-1998

C;Accession: S74196

R;Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Inokuchi, H.

Eur. J. Biochem. 230, 760-765, 1995

A;Title: Induction of terminal enzymes for heme biosynthesis during differentiation of mouse erythroleukemia cells.

A;Reference number: S65629; MUID:95331315; PMID:7607249

A;Accession: S74196

A;Molecule type: protein

A;Residues: 1-12 <TAK>

A;Experimental source: liver

Query Match 37.5%; Score 18; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2.5e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
| || |  
Db 1 STVPAVP 7

#### RESULT 32

A59387

VCAM-1 5'UTR binding protein - Rana pipiens (fragment)

C;Species: Rana pipiens

C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001

C;Accession: A59387

R;BANERJEE, H.

submitted to the Protein Sequence Database, February 2001

A;Description: Identification and characterization of a novel VCAM-1 5'UTR.

A;Reference number: A59387

A;Accession: A59387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <BAN>



A;Experimental source: CCL-145

A;Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibitory effect

Query Match 37.5%; Score 18; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
:| | |  
Db 1 IPLDP 5

#### RESULT 33

PH0805

T-cell receptor alpha chain (PE5.1.1V-alpha-2.8I) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PH0805

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0805

A;Molecule type: mRNA

A;Residues: 1-13 <CAS>

A;Cross-references: EMBL:X60914

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 37.5%; Score 18; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8  
:| | |  
Db 7 NYKPTF 12

#### RESULT 34

I77387

AMP deaminase - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I77387

R;Mineo, I.; Clarke, P.R.H.; Sabina, R.L.; Holmes, E.W.

Mol. Cell. Biol. 10, 5271-5278, 1990

A;Title: A novel pathway for alternative splicing: Identification of an RNA intermediate that generates an alternative 5' splice donor site not present in the primary transcript of AMPD1.

A;Reference number: I57509; MUID:90377216; PMID:2398891

A;Accession: I77387

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-13 <RES>  
A;Cross-references: GB:M58689; NID:g202877; PIDN:AAA40727.1; PID:g554414  
C;Genetics:  
A;Gene: AMPD1  
A;Introns: 8/1

Query Match 37.5%; Score 18; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLF 8  
:| | |  
Db 1 MPLF 4

RESULT 35

PC4391

cysteine proteinase (EC 3.4.22.-) B - Freesia reflacta ssp. 'Golden leader'  
(fragment)

C;Species: Freesia reflacta ssp. 'Golden leader'

C;Date: 10-Nov-1997 #sequence\_revision 10-Nov-1997 #text\_change 07-May-1999

C;Accession: PC4391

R;Kaneda, M.; Yonezawa, H.; Uchikoba, T.

Biosci. Biotechnol. Biochem. 61, 1554-1559, 1997

A;Title: Purification and characterization of a cysteine protease from corms of  
freesia, Freesia reflacta.

A;Reference number: PC4391; MUID:97480942; PMID:9339558

A;Accession: PC4391

A;Molecule type: protein

A;Residues: 1-13 <KAN>

A;Experimental source: corms

C;Comment: This enzyme plays many proteolytic functions in intracellular and  
extracellular processes such as degradation of storage proteins in germinating  
seeds.

C;Keywords: cysteine proteinase; hydrolase

Query Match 37.5%; Score 18; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YVPLF 8  
| | |  
Db 1 YPPFF 5

RESULT 36

PH1566

cerebrin 30 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999

C;Accession: PH1566

R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
J. Neurochem. 61, 533-540, 1993

A;Title: Micropurification of two human cerebrospinal fluid proteins by high  
performance electrophoresis chromatography.

A;Reference number: PH1566; MUID:93329419; PMID:8336140

A;Accession: PH1566

A;Molecule type: protein  
A;Residues: 1-14 <LEO>

Query Match 37.5%; Score 18; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8  
| |||  
Db 7 SVQPLF 12

RESULT 37

PN0666

dystrophin-associated glycoprotein A3a-V - rabbit (fragment)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0666

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0666

A;Molecule type: protein

A;Residues: 1-14 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 37.5%; Score 18; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPL 7  
| ||  
Db 1 YTPL 4

RESULT 38

C59137

protein Pf3 - golden needle mushroom (fragment)

C;Species: *Flammulina velutipes* (golden needle mushroom)

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C;Accession: C59137

R;Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.

submitted to the Protein Sequence Database, November 1999

A;Description: Differences of proteins expressed in the fruiting dikaryon and the non-fruiting monokaryon of *Flammulina velutipes*.

A;Reference number: A59137

A;Accession: C59137

A;Molecule type: protein

A;Residues: 1-14 <SAK>

Query Match 37.5%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
|||  
Db 8 YVP 10

RESULT 39

LFECF

phe operon leader peptide - Escherichia coli (strain K-12)

N;Alternate names: attenuator peptide

C;Species: Escherichia coli

C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 01-Mar-2002

C;Accession: A03593; B36494; A65038

R;Zurawski, G.; Brown, K.; Killingly, D.; Yanofsky, C.

Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978

A;Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli.

A;Reference number: A03593; MUID:79033820; PMID:360214

A;Accession: A03593

A;Molecule type: DNA

A;Residues: 1-15 <ZUR>

A;Cross-references: GB:V00314; GB:J01658; NID:g42378; PIDN:CAA23600.1; PID:g42379

R;Gavini, N.; Davidson, B.E.

J. Biol. Chem. 265, 21532-21535, 1990

A;Title: pheAo mutants of Escherichia coli have a defective pheA attenuator.

A;Reference number: A36494; MUID:91072346; PMID:2254312

A;Accession: B36494

A;Molecule type: DNA

A;Residues: 1-15 <GAV>

A;Cross-references: GB:M58024; GB:J05694; NID:g147178; PIDN:AAA62783.1; PID:g147180

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: A65038

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-15 <BLAT>

A;Cross-references: GB:AE000346; GB:U00096; NID:g2367141; PIDN:AAC75647.1; PID:g1788950; UWGP:b2598

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: pheL; pheAe

A;Map position: 56 min

C;Superfamily: pheA leader peptide

Query Match 37.5%; Score 18; DB 1; Length 15;

Best Local Similarity 40.0%; Pred. No. 3.1e+03;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLF 8  
::| |  
Db 3 HIPFF 7

RESULT 40

PW0004

chlorophyll a/b-binding protein 24.5K - green alga (*Dunaliella tertiolecta*)  
(fragment)

N;Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein

C;Species: *Dunaliella tertiolecta*

C;Date: 04-Sep-1998 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999

C;Accession: PW0004

R;LaRoche, J.; Bennett, J.; Falkowski, P.G.

Gene 95, 165-171, 1990

A;Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from the unicellular marine chlorophyte, *Dunaliella tertiolecta*.

A;Reference number: JW0040; MUID:91065528; PMID:2249775

A;Accession: PW0004

A;Molecule type: protein

A;Residues: 1-15 <LAR>

C;Superfamily: chlorophyll a/b-binding protein

C;Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 37.5%; Score 18; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVP 6  
|| ||  
Db 1 VEFYGP 6

RESULT 41

PN0665

dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0665

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0665

A;Molecule type: protein

A;Residues: 1-15 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 37.5%; Score 18; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPL 7  
| ||  
Db 1 YTPL 4

RESULT 42

T09741  
 photosystem I chain psaI - upland cotton chloroplast (fragment)  
 C;Species: chloroplast *Gossypium hirsutum* (upland cotton)  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C;Accession: T09741  
 R;Small, R.L.; Ryburn, J.A.; Cronn, R.C.; Seelanan, T.; Wendel, J.F.  
 Am. J. Bot. 85, 1301-1315, 1998  
 A;Title: The tortoise and the hare: choosing between noncoding plastome and  
 nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant  
 group.  
 A;Reference number: Z16323  
 A;Accession: T09741  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-16 <SMA>  
 A;Cross-references: EMBL:AF031581; NID:g2623684; PID:g3723945  
 C;Genetics:  
 A;Gene: psaI  
 A;Genome: chloroplast  
 C;Keywords: chloroplast; photosynthesis; photosystem I

Query Match 37.5%; Score 18; DB 2; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
 :|||  
 Db 11 FVPL 14

RESULT 43  
 S38292  
 30K allergen - rye (fragment)  
 C;Species: *Secale cereale* (rye)  
 C;Date: 19-May-1994 #sequence\_revision 27-Feb-1997 #text\_change 07-May-1999  
 C;Accession: S38292  
 R;Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.  
 Biol. Chem. Hoppe-Seyler 374, 855-861, 1993  
 A;Title: Comparison of four grass pollen species concerning their allergens of  
 grass group V by 2D immunoblotting and microsequencing.  
 A;Reference number: S38288; MUID:94092339; PMID:7505588  
 A;Accession: S38292  
 A;Molecule type: protein  
 A;Residues: 1-16 <PET>

Query Match 37.5%; Score 18; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 | | |  
 Db 5 YAPAAP 10

RESULT 44  
 S17274

ribosomal protein YmL35, mitochondrial, questionable - yeast (*Saccharomyces cerevisiae*) (fragment)

C;Species: *Saccharomyces cerevisiae*

A;Variety: strain 07173

C;Date: 23-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 09-May-1997

C;Accession: S17274

R;Grohmann, L.; Graack, H.R.; Krufft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.

FEBS Lett. 284, 51-56, 1991

A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.

A;Reference number: S17255; MUID:91285106; PMID:2060626

A;Accession: S17274

A;Molecule type: protein

A;Residues: 1-17 <GRO>

C;Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae* S288C.

C;Genetics:

A;Genome: nuclear

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 37.5%; Score 18; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|::|  
Db 12 PVYP 15

#### RESULT 45

I52614

u-plasminogen activator receptor precursor - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000

C;Accession: I52614

R;Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.

Blood 86, 624-635, 1995

A;Title: A conserved TATA-less proximal promoter drives basal transcription from the urokinase-type plasminogen activator receptor gene.

A;Reference number: I52614; MUID:95329719; PMID:7605992

A;Accession: I52614

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-18 <RES>

A;Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4261989

C;Genetics:

A;Gene: uPAR

C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 37.5%; Score 18; DB 2; Length 18;  
Best Local Similarity 75.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|||

## RESULT 46

JP0102

fibrinogen beta chain - duck (fragment)

N;Contains: fibrinopeptide B

C;Species: *Anas platyrhynchos* (domestic duck)

C;Date: 30-Jun-1987 #sequence\_revision 28-Dec-1987 #text\_change 13-Sep-1996

C;Accession: JP0102

R;Min, Y.; Ping, Z.; Yaoshi, Z.

Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 28, 31-35, 1985

A;Title: Purification and primary structures of duck fibrinopeptides A and B.

A;Reference number: A94238

A;Accession: JP0102

A;Molecule type: protein

A;Residues: 1-18 &lt;MIN&gt;

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide ring homology

C;Keywords: blood coagulation; plasma; pyroglutamic acid; sulfoprotein

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;6/Binding site: sulfate (Tyr) (covalent) #status predicted

Query Match 37.5%; Score 18; DB 2; Length 18;

Best Local Similarity 80.0%; Pred. No. 3.8e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESYVP 6

|| ||

Db 11 ESTVP 15

## RESULT 47

A57458

gene Gax protein - mouse (fragment)

C;Species: *Mus sp.* (mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Oct-1999

C;Accession: A57458

R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.

Mol. Cell. Biol. 15, 4272-4281, 1995

A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.

A;Reference number: A57458; MUID:95349593; PMID:7623821

A;Accession: A57458

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 &lt;RES&gt;

A;Cross-references: GB:S79168; NID:g1050991

C;Genetics:

A;Gene: Gax

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 35.4%; Score 17; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 6 PLF 8  
|||  
Db 4 PLF 6

RESULT 48

A58838

hemolysin - Porphyromonas gingivalis (fragment)

C;Species: Porphyromonas gingivalis

C;Date: 29-Sep-1999 #sequence\_revision 29-Sep-1999 #text\_change 29-Sep-1999

C;Accession: A58838

R;Deshpande, R.

submitted to the Protein Sequence Database, April 1998

A;Reference number: A58838

A;Accession: A58838

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DES>

Query Match 35.4%; Score 17; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 3.5e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
|:|  
Db 2 YIP 4

RESULT 49

JU0356

cycloleonurinin - sagebrush motherwort

C;Species: Leonurus artemisia (sagebrush motherwort)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C;Accession: JU0356

R;Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.  
Chem. Pharm. Bull. 39, 712-715, 1991

A;Title: Cycloleonurinin, a cyclic peptide from Leonuri fructus.

A;Reference number: JU0356; MUID:91300597; PMID:2070452

A;Accession: JU0356

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KIN>

Query Match 35.4%; Score 17; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
| | |  
Db 1 YTPAGP 6

RESULT 50

S78766

ribosomal protein MRP-S28, mitochondrial - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C;Accession: S78766  
R;Graack, H.R.  
submitted to the Protein Sequence Database, July 1999  
A;Reference number: S78760  
A;Accession: S78766  
A;Molecule type: protein  
A;Residues: 1-13 <GRA>  
C;Keywords: mitochondrion  
F;1-13/Product: ribosomal protein MRP-S28 (fragment) #status experimental <MAT>

Query Match 35.4%; Score 17; DB 2; Length 13;  
Best Local Similarity 42.9%; Pred. No. 4.2e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPL 7  
|||: :  
Db 6 VESFASM 12

Search completed: July 4, 2004, 04:47:20  
Job time : 7.91791 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 17.6642 Seconds  
(without alignments)  
158.601 Million cell updates/sec

Title: US-09-641-802-31  
Perfect score: 48  
Sequence: 1 VESYVPLFP 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	48	100.0	9	14	US-10-281-652-31	Sequence 31, Appl
2	33	68.8	15	10	US-09-880-748-2310	Sequence 2310, Ap
3	33	68.8	15	12	US-10-293-418-2310	Sequence 2310, Ap
4	33	68.8	16	10	US-09-880-748-2263	Sequence 2263, Ap
5	33	68.8	16	12	US-10-293-418-2263	Sequence 2263, Ap
6	29	60.4	10	9	US-09-767-460-64	Sequence 64, Appl
7	29	60.4	13	9	US-09-764-868-1240	Sequence 1240, Ap
8	29	60.4	13	10	US-09-955-999-120	Sequence 120, App
9	29	60.4	14	10	US-09-880-748-2657	Sequence 2657, Ap
10	29	60.4	14	12	US-10-293-418-2657	Sequence 2657, Ap
11	28	58.3	10	9	US-09-767-460-93	Sequence 93, Appl
12	28	58.3	17	14	US-10-161-791-446	Sequence 446, App
13	28	58.3	17	14	US-10-161-791-447	Sequence 447, App
14	27	56.2	11	10	US-09-906-393A-5	Sequence 5, Appli
15	27	56.2	12	16	US-10-264-309-304	Sequence 304, App
16	26	54.2	11	9	US-09-766-378A-30	Sequence 30, Appl
17	26	54.2	14	10	US-09-880-748-2533	Sequence 2533, Ap
18	26	54.2	14	10	US-09-880-748-2710	Sequence 2710, Ap
19	26	54.2	14	12	US-10-293-418-2533	Sequence 2533, Ap
20	26	54.2	14	12	US-10-293-418-2710	Sequence 2710, Ap
21	26	54.2	15	14	US-10-281-478-74	Sequence 74, Appl
22	26	54.2	16	10	US-09-880-748-2261	Sequence 2261, Ap
23	26	54.2	16	12	US-10-293-418-2261	Sequence 2261, Ap
24	26	54.2	18	9	US-09-820-296-5	Sequence 5, Appli
25	26	54.2	18	10	US-09-820-096B-5	Sequence 5, Appli
26	25	52.1	7	12	US-10-258-146A-144	Sequence 144, App
27	25	52.1	7	12	US-10-328-953-289	Sequence 289, App
28	25	52.1	7	14	US-10-052-578-286	Sequence 286, App
29	25	52.1	7	14	US-10-053-520-286	Sequence 286, App
30	25	52.1	7	14	US-10-053-498B-286	Sequence 286, App
31	25	52.1	7	16	US-10-258-144-179	Sequence 179, App
32	25	52.1	8	12	US-10-328-953-126	Sequence 126, App
33	25	52.1	8	14	US-10-052-578-82	Sequence 82, Appl
34	25	52.1	8	14	US-10-053-520-82	Sequence 82, Appl
35	25	52.1	8	14	US-10-053-498B-82	Sequence 82, Appl
36	25	52.1	14	14	US-10-028-075B-108	Sequence 108, App
37	25	52.1	14	14	US-10-029-206A-108	Sequence 108, App
38	25	52.1	15	14	US-10-161-791-379	Sequence 379, App
39	25	52.1	15	14	US-10-239-423-55	Sequence 55, Appl
40	25	52.1	15	14	US-10-275-707-16	Sequence 16, Appl
41	25	52.1	15	16	US-10-432-422-69	Sequence 69, Appl
42	25	52.1	15	16	US-10-432-422-70	Sequence 70, Appl
43	25	52.1	17	14	US-10-331-907-403	Sequence 403, App
44	24	50.0	7	9	US-09-758-128-45	Sequence 45, Appl
45	24	50.0	7	9	US-09-758-426-45	Sequence 45, Appl
46	24	50.0	7	9	US-09-758-198-45	Sequence 45, Appl
47	24	50.0	7	10	US-09-861-661-45	Sequence 45, Appl
48	24	50.0	9	12	US-10-253-286-464	Sequence 464, App
49	24	50.0	9	15	US-10-245-871-464	Sequence 464, App
50	24	50.0	9	15	US-10-408-133-16	Sequence 16, Appl
51	24	50.0	10	14	US-10-235-483-10	Sequence 10, Appl
52	24	50.0	11	9	US-09-760-899-1	Sequence 1, Appli
53	24	50.0	11	12	US-10-376-286-1	Sequence 1, Appli
54	24	50.0	11	14	US-10-239-313A-268	Sequence 268, App
55	24	50.0	12	16	US-10-685-898-32	Sequence 32, Appl
56	24	50.0	14	10	US-09-880-748-2349	Sequence 2349, Ap

57	24	50.0	14	10	US-09-880-748-2388	Sequence 2388, Ap
58	24	50.0	14	10	US-09-880-748-2423	Sequence 2423, Ap
59	24	50.0	14	10	US-09-880-748-2447	Sequence 2447, Ap
60	24	50.0	14	10	US-09-880-748-2467	Sequence 2467, Ap
61	24	50.0	14	10	US-09-880-748-2640	Sequence 2640, Ap
62	24	50.0	14	10	US-09-880-748-2689	Sequence 2689, Ap
63	24	50.0	14	12	US-10-293-418-2349	Sequence 2349, Ap
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65	24	50.0	14	12	US-10-293-418-2423	Sequence 2423, Ap
66	24	50.0	14	12	US-10-293-418-2447	Sequence 2447, Ap
67	24	50.0	14	12	US-10-293-418-2467	Sequence 2467, Ap
68	24	50.0	14	12	US-10-293-418-2640	Sequence 2640, Ap
69	24	50.0	14	12	US-10-293-418-2689	Sequence 2689, Ap
70	24	50.0	14	14	US-10-057-789-49	Sequence 49, Appl
71	24	50.0	14	14	US-10-212-628-49	Sequence 49, Appl
72	24	50.0	15	14	US-10-161-791-319	Sequence 319, App
73	24	50.0	15	16	US-10-203-915A-17	Sequence 17, Appl
74	24	50.0	15	16	US-10-203-915A-18	Sequence 18, Appl
75	24	50.0	15	16	US-10-203-915A-19	Sequence 19, Appl
76	24	50.0	16	9	US-09-947-258-1	Sequence 1, Appli
77	24	50.0	16	9	US-09-947-258-4	Sequence 4, Appli
78	24	50.0	16	10	US-09-880-748-2307	Sequence 2307, Ap
79	24	50.0	16	12	US-10-293-418-2307	Sequence 2307, Ap
80	24	50.0	16	14	US-10-057-789-51	Sequence 51, Appl
81	24	50.0	16	14	US-10-057-789-75	Sequence 75, Appl
82	24	50.0	16	14	US-10-212-628-51	Sequence 51, Appl
83	24	50.0	16	14	US-10-212-628-75	Sequence 75, Appl
84	24	50.0	16	14	US-10-225-567A-845	Sequence 845, App
85	24	50.0	18	9	US-09-789-561-189	Sequence 189, App
86	24	50.0	18	14	US-10-161-791-305	Sequence 305, App
87	23	47.9	9	14	US-10-062-109A-595	Sequence 595, App
88	23	47.9	9	14	US-10-062-109A-666	Sequence 666, App
89	23	47.9	9	14	US-10-005-480A-595	Sequence 595, App
90	23	47.9	9	14	US-10-005-480A-666	Sequence 666, App
91	23	47.9	10	14	US-10-062-710-208	Sequence 208, App
92	23	47.9	10	15	US-10-350-367-31	Sequence 31, Appl
93	23	47.9	11	9	US-09-736-076-24	Sequence 24, Appl
94	23	47.9	11	9	US-09-736-076-66	Sequence 66, Appl
95	23	47.9	11	13	US-10-032-330-3	Sequence 3, Appli
96	23	47.9	11	13	US-10-032-330-10	Sequence 10, Appl
97	23	47.9	12	9	US-09-766-412-34	Sequence 34, Appl
98	23	47.9	12	12	US-09-990-747-21	Sequence 21, Appl
99	23	47.9	12	14	US-10-012-363A-10	Sequence 10, Appl
100	23	47.9	12	14	US-10-075-869-45	Sequence 45, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-281-652-31

; Sequence 31, Application US/10281652

; Publication No. US20030091606A1

##### ; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

```

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-31

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Query Match          100.0%; Score 48; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 VESYVPLFP 9
        |||||
Db      1 VESYVPLFP 9

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# RESULT 2

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US-09-880-748-2310
; Sequence 2310, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2310
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2310

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Query Match 68.8%; Score 33; DB 10; Length 15;  
Best Local Similarity 85.7%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
|||||  
Db 8 SYVPLLP 14

RESULT 3

US-10-293-418-2310  
; Sequence 2310, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2310  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2310

Query Match 68.8%; Score 33; DB 12; Length 15;  
Best Local Similarity 85.7%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
|||||  
Db 8 SYVPLLP 14

RESULT 4

US-09-880-748-2263  
; Sequence 2263, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.

```

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2263
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2263

```

```

Query Match          68.8%; Score 33; DB 10; Length 16;
Best Local Similarity 85.7%; Pred. No. 26;
Matches      6; Conservative    0; Mismatches    1; Indels      0; Gaps      0;

```

```

Qy      3 SYVPLFP 9
        ||||| |
Db      8 SYVPLLP 14

```

# RESULT 5

US-10-293-418-2263

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; Sequence 2263, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:

```

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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16

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; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2263  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2263

Query Match 68.8%; Score 33; DB 12; Length 16;  
Best Local Similarity 85.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
|||||  
Db 8 SYVPLLP 14

RESULT 6

US-09-767-460-64

; Sequence 64, Application US/09767460  
; Patent No. US20020009756A1  
; GENERAL INFORMATION:  
; APPLICANT: Mandell, Arnold  
; APPLICANT: Selz, Karen  
; APPLICANT: Shlesinger, Michael  
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or  
Modulation of the  
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
; FILE REFERENCE: 01561-0002-CPUS01  
; CURRENT APPLICATION NUMBER: US/09/767,460  
; CURRENT FILING DATE: 2001-01-23  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 64  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-767-460-64

Query Match 60.4%; Score 29; DB 9; Length 10;  
Best Local Similarity 55.6%; Pred. No. 88;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|::| ||  
Db 1 VQTYPPHFP 9

RESULT 7

US-09-764-868-1240

; Sequence 1240, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ32

; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1240  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-868-1240

Query Match 60.4%; Score 29; DB 9; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
| | | | : |  
Db 1 SYVPMSP 7

RESULT 8

US-09-955-999-120  
; Sequence 120, Application US/09955999  
; Publication No. US20030036505A1  
; GENERAL INFORMATION:  
; APPLICANT: Barash et al.  
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides,  
Polypeptides,  
; TITLE OF INVENTION: Antibodies, and Methods Based Thereon  
; FILE REFERENCE: PT086P1  
; CURRENT APPLICATION NUMBER: US/09/955,999  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 120  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-999-120

Query Match 60.4%; Score 29; DB 10; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
| | | | : |  
Db 1 SYVPMSP 7

RESULT 9

US-09-880-748-2657  
; Sequence 2657, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.

```

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2657
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2657

```

```

Query Match          60.4%;  Score 29;  DB 10;  Length 14;
Best Local Similarity 83.3%;  Pred. No. 1.3e+02;
Matches      5;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

```

```

Qy      4 YVPLFP 9
        | |||
Db      9 YSPLFP 14

```

# RESULT 10

US-10-293-418-2657

```

; Sequence 2657, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16

```

; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2657  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2657

Query Match 60.4%; Score 29; DB 12; Length 14;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
| | | |  
Db 9 YSPLFP 14

RESULT 11

US-09-767-460-93  
; Sequence 93, Application US/09767460  
; Patent No. US20020009756A1  
; GENERAL INFORMATION:  
; APPLICANT: Mandell, Arnold  
; APPLICANT: Selz, Karen  
; APPLICANT: Shlesinger, Michael  
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or  
Modulation of the  
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
; FILE REFERENCE: 01561-0002-CPUS01  
; CURRENT APPLICATION NUMBER: US/09/767,460  
; CURRENT FILING DATE: 2001-01-23  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-767-460-93

Query Match 58.3%; Score 28; DB 9; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
| | | |  
Db 3 SYTPEFP 9

RESULT 12

US-10-161-791-446  
; Sequence 446, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.

```

; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 446:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-446

```

```

Query Match          58.3%; Score 28; DB 14; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches      4; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      2 ESYVPLFP 9
        | |:|: |
Db      6 EWYIPIIP 13

```

```

RESULT 13
US-10-161-791-447
; Sequence 447, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

```

```

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 447:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-447

```

```

Query Match          58.3%; Score 28; DB 14; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      2 ESYVPLFP 9
        | | : | : |
Db      6 EWYIPIIP 13

```

```

RESULT 14
US-09-906-393A-5
; Sequence 5, Application US/09906393A
; Publication No. US20030039970A1

```

; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906,393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-906-393A-5

Query Match 56.2%; Score 27; DB 10; Length 11;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|| |||  
Db 5 YVKLFP 10

RESULT 15

US-10-264-309-304

; Sequence 304, Application US/10264309  
; Publication No. US20040022794A1  
; GENERAL INFORMATION:  
; APPLICANT: DURHAM, L. KATHRYN  
; APPLICANT: FRIEDMAN, DAVID L.  
; APPLICANT: HERATH, HERATH  
; APPLICANT: KIMMEL, LIDA H.  
; APPLICANT: PAREKH, RAJESH B.  
; APPLICANT: POTTER, DAVID M.  
; APPLICANT: ROHLFF, CHRISTIAN  
; APPLICANT: SILBER, B. MICHAEL  
; APPLICANT: SNYDER, PETER J.  
; APPLICANT: SOARES, HOLLY D.  
; APPLICANT: STIGER, THOMAS R.  
; APPLICANT: SUNDERLAND, P. TREY  
; APPLICANT: TOWNSEND, ROBERT R.  
; APPLICANT: WHITE, W. FROST  
; APPLICANT: WILLIAMS, STEPHEN A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,  
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
; FILE REFERENCE: POA-002.01  
; CURRENT APPLICATION NUMBER: US/10/264,309  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: 60/326,708  
; PRIOR FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO 304  
; LENGTH: 12

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-309-304

Query Match 56.2%; Score 27; DB 16; Length 12;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VESYVP 6  
| | | | |  
Db 2 VESYTP 7

RESULT 16

US-09-766-378A-30

; Sequence 30, Application US/09766378A  
; Patent No. US20020091079A1

; GENERAL INFORMATION:

; APPLICANT: Rhode, Peter R.  
; Acevedo, Jorge  
; Burkhardt, Martin  
; Jiao, Jin-an  
; Wong, Hing C.

; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND  
; METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: usa  
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/766,378A  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/960,190  
; FILING DATE: 29-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 48002-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids  
; TYPE: amino acid



; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-766-378A-30

Query Match 54.2%; Score 26; DB 9; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ESYVPLFP 9  
| | : | : |  
Db 3 EYMPMEP 10

RESULT 17

US-09-880-748-2533  
; Sequence 2533, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2533  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2533

Query Match 54.2%; Score 26; DB 10; Length 14;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVPLFP 9  
: | | | |  
Db 9 HAPLFP 14

RESULT 18

US-09-880-748-2710  
; Sequence 2710, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:

```

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2710
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-2710

```

```

Query Match          54.2%;  Score 26;  DB 10;  Length 14;
Best Local Similarity 66.7%;  Pred. No. 4.5e+02;
Matches      4;  Conservative    1;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy      4 YVPLFP 9
        | ||:|
Db      9 YSPLYP 14

```

# RESULT 19

```

US-10-293-418-2533
; Sequence 2533, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210

```

; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2533  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2533

Query Match 54.2%; Score 26; DB 12; Length 14;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
: ||||  
Db 9 HAPLFP 14

RESULT 20

US-10-293-418-2710  
; Sequence 2710, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2710  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2710

Query Match 54.2%; Score 26; DB 12; Length 14;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
| ||:|  
Db 9 YSPLYP 14

RESULT 21

US-10-281-478-74

```
; Sequence 74, Application US/10281478
; Publication No. US20030108959A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Johnson, Richard S.
; APPLICANT: Guo, Lin
; APPLICANT: Mahimkar, Rajeev M.
; APPLICANT: Peschon, Jacques J.
; APPLICANT: Black, Roy A.
; TITLE OF INVENTION: TREATING DISEASES MEDIATED BY METALLOPROTEASE-SHED
PROTEINS
; FILE REFERENCE: 3327-A
; CURRENT APPLICATION NUMBER: US/10/281,478
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: methionine sulfoxide
US-10-281-478-74
```

```
Query Match          54.2%; Score 26; DB 14; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches      4; Conservative      3; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 VESYVPL 7
        |:|:|:
Db      3 VDSYLPV 9
```

RESULT 22

US-09-880-748-2261

```
; Sequence 2261, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
```

; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2261  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2261

Query Match 54.2%; Score 26; DB 10; Length 16;  
Best Local Similarity 71.4%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
| | | | |  
Db 8 SYVPCSP 14

RESULT 23

US-10-293-418-2261

; Sequence 2261, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2261  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2261

Query Match 54.2%; Score 26; DB 12; Length 16;  
Best Local Similarity 71.4%; Pred. No. 5.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
 |||| |  
Db 8 SYVPCSP 14

RESULT 24

US-09-820-296-5

; Sequence 5, Application US/09820296  
; Patent No. US20010048424A1  
; GENERAL INFORMATION:  
; APPLICANT: Kasahara, Hiroyuki  
; APPLICANT: Davin, Laurence  
; APPLICANT: Lewis, No. US20010048424Alman  
; TITLE OF INVENTION: ARYL PROPENAL DOUBLE BOND REDUCTASE  
; FILE REFERENCE: WSUR-1-17233  
; CURRENT APPLICATION NUMBER: US/09/820,296  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/192,266  
; PRIOR FILING DATE: 2000-03-27  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Pinus Taeda  
US-09-820-296-5

Query Match 54.2%; Score 26; DB 9; Length 18;  
Best Local Similarity 66.7%; Pred. No. 5.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 |:| ||  
Db 7 YLPSFP 12

RESULT 25

US-09-820-096B-5

; Sequence 5, Application US/09820096B  
; Publication No. US20030022168A1  
; GENERAL INFORMATION:  
; APPLICANT: Kasahara, Hiroyuki  
; APPLICANT: Davin, Laurence  
; APPLICANT: Lewis, No. US20030022168Alman  
; TITLE OF INVENTION: ARYL PROPENAL DOUBLE BOND REDUCTASE  
; FILE REFERENCE: WSUR-1-17233  
; CURRENT APPLICATION NUMBER: US/09/820,096B  
; CURRENT FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,266  
; PRIOR FILING DATE: 2000-03-27  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Pinus Taeda

US-09-820-096B-5

Query Match 54.2%; Score 26; DB 10; Length 18;  
Best Local Similarity 66.7%; Pred. No. 5.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|:| ||  
Db 7 YLPSFP 12

RESULT 26

US-10-258-146A-144

; Sequence 144, Application US/10258146A  
; Publication No. US20040052812A1  
; GENERAL INFORMATION:  
; APPLICANT: Mee Hoe  
; APPLICANT: Frank Landsberger  
; TITLE OF INVENTION: HEAT SHOCK PROTEIN-BASED ANTIVIRAL  
; TITLE OF INVENTION: VACCINES  
; FILE REFERENCE: 11390/46301  
; CURRENT APPLICATION NUMBER: US/10/258,146A  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: PCT/US01/12568  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/197,462  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 144  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: obtained from a phage synthetic peptide library  
US-10-258-146A-144

Query Match 52.1%; Score 25; DB 12; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|||| |  
Db 2 YVPLPP 7

RESULT 27

US-10-328-953-289

; Sequence 289, Application US/10328953  
; Publication No. US20040071656A1  
; GENERAL INFORMATION:  
; APPLICANT: Wieland, Felix  
; APPLICANT: Hartl, Franz-Ulrich  
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies  
; FILE REFERENCE: 11390/46101  
; CURRENT APPLICATION NUMBER: US/10/328,953  
; CURRENT FILING DATE: 2002-12-23

```
; PRIOR APPLICATION NUMBER: US 60/342,570
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: US 60/343,884
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/372,620
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/399,342
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/414,834
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 289
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-328-953-289
```

```
Query Match          52.1%; Score 25; DB 12; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches      5; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy          4 YVPLFP 9
             |||||
Db          2 YVPLPP 7
```

```
RESULT 28
US-10-052-578-286
; Sequence 286, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-052-578-286
```



Query Match 52.1%; Score 25; DB 14; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|||||  
Db 2 YVPLPP 7

RESULT 29

US-10-053-520-286

; Sequence 286, Application US/10053520  
; Publication No. US20030166530A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Ouerfelli, Ouathak  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46004  
; CURRENT APPLICATION NUMBER: US/10/053,520  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 286  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-053-520-286

Query Match 52.1%; Score 25; DB 14; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|||||  
Db 2 YVPLPP 7

RESULT 30

US-10-053-498B-286

; Sequence 286, Application US/10053498B  
; Publication No. US20030194409A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.

```
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-286
```

```
Query Match          52.1%; Score 25; DB 14; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches      5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 YVPLFP 9
        |||||
Db      2 YVPLPP 7
```

```
RESULT 31
US-10-258-144-179
; Sequence 179, Application US/10258144
; Publication No. US20040101532A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Alan
; APPLICANT: Livingston, Phil
; APPLICANT: Al-Awqati, Qais
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT SHOCK
; TITLE OF INVENTION: PROTEIN MEDIATED IMMUNOTHERAPY OF MELANOMA
; FILE REFERENCE: 11746/46401
; CURRENT APPLICATION NUMBER: US/10/258,144
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/197,642
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 502
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ml3 coliphage insert
US-10-258-144-179
```

```
Query Match          52.1%; Score 25; DB 16; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches      5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 4 YVPLFP 9  
 |||| |  
Db 2 YVPLPP 7

RESULT 32

US-10-328-953-126

; Sequence 126, Application US/10328953  
; Publication No. US20040071656A1  
; GENERAL INFORMATION:  
; APPLICANT: Wieland, Felix  
; APPLICANT: Hartl, Franz-Ulrich  
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies  
; FILE REFERENCE: 11390/46101  
; CURRENT APPLICATION NUMBER: US/10/328,953  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 60/342,570  
; PRIOR FILING DATE: 2001-12-26  
; PRIOR APPLICATION NUMBER: US 60/343,884  
; PRIOR FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 60/372,620  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 60/399,342  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: US 60/414,834  
; PRIOR FILING DATE: 2002-09-28  
; NUMBER OF SEQ ID NOS: 331  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 126  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-328-953-126

Query Match 52.1%; Score 25; DB 12; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 |||| |  
Db 2 YVPLPP 7

RESULT 33

US-10-052-578-82

; Sequence 82, Application US/10052578  
; Publication No. US20030134787A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich

```
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-052-578-82
```

```
Query Match          52.1%; Score 25; DB 14; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches      5; Conservative    0; Mismatches    1; Indels      0; Gaps      0;
```

```
Qy      4 YVPLFP 9
        |||| |
Db      2 YVPLPP 7
```

#### RESULT 34

```
US-10-053-520-82
; Sequence 82, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-82
```

```
Query Match          52.1%; Score 25; DB 14; Length 8;
```

Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|||||  
Db 2 YVPLPP 7

RESULT 35

US-10-053-498B-82

; Sequence 82, Application US/10053498B

; Publication No. US20030194409A1

; GENERAL INFORMATION:

; APPLICANT: Sloan-Kettering Institute for Cancer Research

; APPLICANT: Rothman, James E.

; APPLICANT: Mayhew, Mark

; APPLICANT: Hoe, Mee H.

; APPLICANT: Houghton, Alan

; APPLICANT: Hartl, Ulrich

; APPLICANT: Ouerfelli, Ouathak

; APPLICANT: Moroi, Yoichi

; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES

; FILE REFERENCE: 11746/46002

; CURRENT APPLICATION NUMBER: US/10/053,498B

; CURRENT FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 08/961,707

; PRIOR FILING DATE: 1997-10-31

; NUMBER OF SEQ ID NOS: 321

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 82

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: peptide in m13 coliphage

US-10-053-498B-82

Query Match 52.1%; Score 25; DB 14; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
|||||  
Db 2 YVPLPP 7

RESULT 36

US-10-028-075B-108

; Sequence 108, Application US/10028075B

; Publication No. US20030113733A1

; GENERAL INFORMATION:

; APPLICANT: Khan, Nisar A.

; APPLICANT: Benner, Robert

; TITLE OF INVENTION: Gene regulator

; FILE REFERENCE: 2183-5223US

; CURRENT APPLICATION NUMBER: US/10/028,075B

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 108  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Mm.129320.2  
US-10-028-075B-108

Query Match 52.1%; Score 25; DB 14; Length 14;  
Best Local Similarity 44.4%; Pred. No. 6.9e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|: ||: |  
Db 2 VQKVVPMPLP 10

RESULT 37

US-10-029-206A-108  
; Sequence 108, Application US/10029206A  
; Publication No. US20030119720A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Oligopeptide treatment of anthrax  
; FILE REFERENCE: 2183-5222US  
; CURRENT APPLICATION NUMBER: US/10/029,206A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/821,380  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 108  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Mm.129320.2  
US-10-029-206A-108

Query Match 52.1%; Score 25; DB 14; Length 14;  
Best Local Similarity 44.4%; Pred. No. 6.9e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|: ||: |  
Db 2 VQKVVPMPLP 10

RESULT 38

US-10-161-791-379  
; Sequence 379, Application US/10161791  
; Publication No. US20030186863A1

```

; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-379

```

```

Query Match          52.1%; Score 25; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 7.4e+02;
Matches      4; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          5 VPLFP 9
             :||||
Db          7 LPLFP 11

```

```

RESULT 39
US-10-239-423-55

```

```
; Sequence 55, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells
and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine ..
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand
Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-55
```

```
Query Match          52.1%; Score 25; DB 14; Length 15;
Best Local Similarity 60.0%; Pred. No. 7.4e+02;
Matches      3; Conservative      2; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 VPLFP 9
        :|:|
Db      2 IPIFP 6
```

#### RESULT 40

US-10-275-707-16

```
; Sequence 16, Application US/10275707
; Publication No. US20030194801A1
; GENERAL INFORMATION:
; APPLICANT: BONALDO, MIRNA C.
; APPLICANT: GALLER, RICARDO
; APPLICANT: FREIRE, MARCOS DA SILVA
; APPLICANT: GARRAT, RICHARD C.
; TITLE OF INVENTION: USE OF FLAVIVIRUS FOR THE EXPRESSION OF PROTEIN EPITOPES
; TITLE OF INVENTION: AND DEVELOPMENT OF NEW LIVE ATTENUATED VACCINE VIRUS TO
; TITLE OF INVENTION: IMMUNIZE AGAINST FLAVIVIRUS AND OTHER INFECTIOUS AGENTS
; FILE REFERENCE: 3673-21
; CURRENT APPLICATION NUMBER: US/10/275,707
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/BR02/00036
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: GB 0105877.5
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 16
```



; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Plasmodium yoelii  
US-10-275-707-16

Query Match 52.1%; Score 25; DB 14; Length 15;  
Best Local Similarity 66.7%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYVP 6  
::||||  
Db 2 MDSYVP 7

RESULT 41

US-10-432-422-69  
; Sequence 69, Application US/10432422  
; Publication No. US20040076981A1  
; GENERAL INFORMATION:  
; APPLICANT: Syngenta Participations AG  
; APPLICANT: Cornell Research Foundation, Inc.  
; APPLICANT: Yoder, Olen  
; APPLICANT: Turgeon, Barbara G.  
; APPLICANT: Lu, Shen-wen  
; TITLE OF INVENTION: Fungal Iron Reductase Gene  
; FILE REFERENCE: 1360.017W01  
; CURRENT APPLICATION NUMBER: US/10/432,422  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/252,732  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 60/252,649  
; PRIOR FILING DATE: 2000-11-22  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Aspergillus nidulans  
US-10-432-422-69

Query Match 52.1%; Score 25; DB 16; Length 15;  
Best Local Similarity 57.1%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
:||||: |  
Db 7 AYVPIDP 13

RESULT 42

US-10-432-422-70  
; Sequence 70, Application US/10432422  
; Publication No. US20040076981A1  
; GENERAL INFORMATION:  
; APPLICANT: Syngenta Participations AG

; APPLICANT: Cornell Research Foundation, Inc.  
; APPLICANT: Yoder, Olen  
; APPLICANT: Turgeon, Barbara G.  
; APPLICANT: Lu, Shen-wen  
; TITLE OF INVENTION: Fungal Iron Reductase Gene  
; FILE REFERENCE: 1360.017W01  
; CURRENT APPLICATION NUMBER: US/10/432,422  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/252,732  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 60/252,649  
; PRIOR FILING DATE: 2000-11-22  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Aspergillus nidulans  
US-10-432-422-70

Query Match 52.1%; Score 25; DB 16; Length 15;  
Best Local Similarity 57.1%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
:| | | : |  
Db 7 AYVPIDP 13

RESULT 43

US-10-331-907-403

; Sequence 403, Application US/10331907  
; Publication No. US20030181660A1  
; GENERAL INFORMATION:  
; APPLICANT: Todd, John A  
; Hess, John W  
; Caskey, Charles T  
; Cox, Roger D  
; Gerhold, David  
; Hammond, Holly  
; Hey, Patricia  
; Kawaguchi, Yoshihiko  
; Merriman, Tony R  
; Metzker, Michael L  
; TITLE OF INVENTION: No. US20030181660A1el LDL-Receptor  
; NUMBER OF SEQUENCES: 455  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon and Vanderhye  
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: VA 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;      SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/331,907
;      FILING DATE: 31-Dec-2002
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/402,923A
;      FILING DATE: 14-Feb-2001
;      APPLICATION NUMBER: PCT/GB98/01102
;      FILING DATE: 15-APR-1998
;      APPLICATION NUMBER: US 60/043,553
;      FILING DATE: 15-APR-1997
;      APPLICATION NUMBER: US 60/048,740
;      FILING DATE: 05-JUN-1997
;      ATTORNEY/AGENT INFORMATION:
;      NAME: B.J.Sadoff
;      REGISTRATION NUMBER: 36,663
;      REFERENCE/DOCKET NUMBER: 620-81
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (703)816-4091
;      TELEFAX: (703)816-4100
;      INFORMATION FOR SEQ ID NO: 403:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 17 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-10-331-907-403

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Query Match          52.1%; Score 25; DB 14; Length 17;
Best Local Similarity 71.4%; Pred. No. 8.4e+02;
Matches      5; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

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Qy      3 SYVPLFP 9
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Db      1 SYFHLFP 7

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RESULT 44
US-09-758-128-45
; Sequence 45, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45

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; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-128-45

Query Match 50.0%; Score 24; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||||  
Db 3 PLFP 6

RESULT 45

US-09-758-426-45

; Sequence 45, Application US/09758426  
; Patent No. US20020169116A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020169116A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,426  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-426-45

Query Match 50.0%; Score 24; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||||  
Db 3 PLFP 6

RESULT 46

US-09-758-198-45

; Sequence 45, Application US/09758198  
; Publication No. US20020187925A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020187925A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

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; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-198-45

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```

Query Match          50.0%; Score 24; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      6 PLFP 9
        ||||
Db      3 PLFP 6

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#### RESULT 47

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US-09-861-661-45
; Sequence 45, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-45

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Query Match          50.0%; Score 24; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      6 PLFP 9
        ||||

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Db 3 PLFP 6

RESULT 48

US-10-253-286-464

; Sequence 464, Application US/10253286  
; Publication No. US20040058881A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2015  
; CURRENT APPLICATION NUMBER: US/10/253,286  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 464  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-286-464

Query Match 50.0%; Score 24; DB 12; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
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Db 3 VPFFP 7

RESULT 49

US-10-245-871-464

; Sequence 464, Application US/10245871  
; Publication No. US20030235594A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2013  
; CURRENT APPLICATION NUMBER: US/10/245,871  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 464  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-245-871-464

Query Match 50.0%; Score 24; DB 15; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
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Db 3 VPFFP 7

RESULT 50

US-10-408-133-16

; Sequence 16, Application US/10408133

; Publication No. US20040018173A1

; GENERAL INFORMATION:

; APPLICANT: Thompson, Timothy C

; APPLICANT: Ren, Chengzen

; TITLE OF INVENTION: Compositions and Methods for the Treatment and Prevention  
of Metastatic

; TITLE OF INVENTION: Disorders

; FILE REFERENCE: PRO025/4-4DIVUS/16000

; CURRENT APPLICATION NUMBER: US/10/408,133

; CURRENT FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 9

; TYPE: PRT

; ORGANISM: homo sapiens sapiens

US-10-408-133-16

Query Match 50.0%; Score 24; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||||  
Db 6 PLFP 9

Search completed: July 4, 2004, 05:12:32

Job time : 18.6642 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 15.3134 Seconds  
(without alignments)  
185.436 Million cell updates/sec

Title: US-09-641-802-31  
Perfect score: 48  
Sequence: 1 VESYVPLFP 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
No.						

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1	26	54.2	18	4	Q9NSF0	Q9nsf0 homo sapien
2	26	54.2	18	5	Q9TWL5	Q9twl5 lucilia cup
3	25	52.1	17	3	Q9URC6	Q9urc6 saccharomyc
4	24	50.0	15	2	Q8RKN0	Q8rkn0 escherichia
5	24	50.0	16	10	O82407	O82407 fragaria vi
6	24	50.0	16	10	O82404	O82404 fragaria ni
7	24	50.0	16	10	O82406	O82406 fragaria mo
8	24	50.0	16	10	O82402	O82402 fragaria nu
9	24	50.0	16	10	O82403	O82403 fragaria ve
10	24	50.0	16	10	O82781	O82781 fragaria ve
11	24	50.0	16	10	O82405	O82405 fragaria ii
12	23	47.9	13	8	Q9T2U1	Q9t2u1 bos taurus
13	23	47.9	15	2	Q52135	Q52135 enterococcu
14	23	47.9	18	4	Q9UCL5	Q9ucl5 homo sapien
15	22	45.8	15	10	Q9S8V7	Q9s8v7 triticum ae
16	22	45.8	15	12	Q69353	Q69353 herpes simp
17	21	43.8	11	8	Q32704	Q32704 nicotiana t
18	21	43.8	12	12	Q83139	Q83139 barley stri
19	21	43.8	13	13	P82881	P82881 rana clamit
20	21	43.8	16	6	Q9BGG8	Q9bgg8 sorex arane
21	21	43.8	16	11	O54894	O54894 mus musculu
22	21	43.8	17	4	Q9HB76	Q9hb76 homo sapien
23	21	43.8	18	8	Q85UU5	Q85uu5 anthoceros
24	21	43.8	18	10	Q41458	Q41458 solanum tub
25	20	41.7	11	2	Q56972	Q56972 yersinia pe
26	20	41.7	15	11	O88175	O88175 mus musculu
27	20	41.7	16	12	Q9WMG6	Q9wmg6 sigma virus
28	19	39.6	9	10	Q9S8J8	Q9s8j8 oryza sativ
29	19	39.6	13	3	Q96WW8	Q96ww8 geotrichum
30	19	39.6	14	4	Q9P2A2	Q9p2a2 homo sapien
31	19	39.6	14	11	O70599	O70599 rattus norv
32	19	39.6	17	4	Q9NY39	Q9ny39 homo sapien
33	19	39.6	17	8	Q7YAT7	Q7yat7 cooperia on
34	19	39.6	17	8	Q7Y834	Q7y834 cooperia on
35	19	39.6	17	11	Q9QVH7	Q9qvh7 rattus sp.
36	19	39.6	18	5	Q7YXH4	Q7yxh4 caenorhabdi
37	19	39.6	18	17	Q8ZSZ9	Q8zsz9 pyrobaculum
38	18	37.5	9	3	Q9P8E5	Q9p8e5 kluveromyc
39	18	37.5	9	12	Q88612	Q88612 middelburg
40	18	37.5	12	6	Q9TRY4	Q9try4 sus sp. ins
41	18	37.5	13	11	Q63047	Q63047 rattus norv
42	18	37.5	13	13	Q9PVA0	Q9pva0 colisa lali
43	18	37.5	13	13	Q9PVB1	Q9pvb1 dendrochiru
44	18	37.5	13	13	Q9PV95	Q9pv95 mola mola (
45	18	37.5	13	13	Q9PVA7	Q9pva7 dissostichu
46	18	37.5	13	13	Q9PVB3	Q9pvb3 hippocampus
47	18	37.5	13	13	Q9PV98	Q9pv98 psettodes s
48	18	37.5	13	13	Q9PV97	Q9pv97 balistes sp
49	18	37.5	13	13	Q9PVB2	Q9pvb2 mastacembel
50	18	37.5	13	13	Q9PVA2	Q9pva2 thunnus sp.
51	18	37.5	13	13	Q9PVB0	Q9pvb0 dicentrarch
52	18	37.5	13	13	Q9PVB4	Q9pvb4 zeus faber
53	18	37.5	13	13	Q9PV99	Q9pv99 channa sp.
54	18	37.5	13	13	Q9PVA5	Q9pva5 cryptocentr
55	18	37.5	13	13	Q9PVA3	Q9pva3 acanthurus
56	18	37.5	13	13	Q9PVA9	Q9pva9 epinephelus
57	18	37.5	13	13	Q9PVC5	Q9pvc5 galaxias ma

58	18	37.5	13	13	Q9PVA4	Q9pva4 siganus sp.
59	18	37.5	13	13	Q9PVA1	Q9pva1 stromateus
60	18	37.5	13	13	Q9PV96	Q9pv96 ostracion s
61	18	37.5	13	13	Q9PVB5	Q9pvb5 sargocentro
62	18	37.5	13	13	Q9PVB7	Q9pvb7 fundulus he
63	18	37.5	13	13	Q9PVB6	Q9pvb6 poecilia la
64	18	37.5	13	13	Q9PVA6	Q9pva6 salarias sp
65	18	37.5	13	13	P82866	P82866 rana pipien
66	18	37.5	14	2	Q8RK22	Q8rk22 pseudomonas
67	18	37.5	15	6	Q9TR45	Q9tr45 bos taurus
68	18	37.5	15	6	Q9TRN8	Q9trn8 sus scrofa
69	18	37.5	15	8	Q85XG6	Q85xg6 clusia arip
70	18	37.5	15	8	Q85XG4	Q85xg4 clusia croa
71	18	37.5	15	8	Q85XG2	Q85xg2 clusia flav
72	18	37.5	15	8	Q85XG0	Q85xg0 clusia flum
73	18	37.5	15	8	Q85XF8	Q85xf8 clusia gran
74	18	37.5	15	8	Q85XF6	Q85xf6 clusia inte
75	18	37.5	15	8	Q85XF4	Q85xf4 clusia lanc
76	18	37.5	15	8	Q85XF2	Q85xf2 clusia majo
77	18	37.5	15	8	Q85XE9	Q85xe9 clusia nemo
78	18	37.5	15	8	Q85XE7	Q85xe7 clusia rose
79	18	37.5	15	8	Q85XE5	Q85xe5 clusia sten
80	18	37.5	15	8	Q85XE3	Q85xe3 clusia tocu
81	18	37.5	15	8	Q85XE1	Q85xe1 clusia torr
82	18	37.5	15	8	Q85XD9	Q85xd9 clusia vale
83	18	37.5	15	8	Q85C69	Q85c69 clusia ducu
84	18	37.5	15	8	Q85C68	Q85c68 clusia mino
85	18	37.5	15	8	Q85C67	Q85c67 clusia mult
86	18	37.5	16	2	Q9R963	Q9r963 helicobacte
87	18	37.5	16	8	O19977	O19977 gossypium m
88	18	37.5	16	8	O19975	O19975 gossypium t
89	18	37.5	16	8	O19973	O19973 gossypium b
90	18	37.5	16	8	O19971	O19971 gossypium h
91	18	37.5	16	11	Q9CW70	Q9cw70 mus musculu
92	18	37.5	18	2	Q8L2T5	Q8l2t5 neisseria m
93	18	37.5	18	3	Q9UR73	Q9ur73 trichoderma
94	18	37.5	18	8	O19979	O19979 gossypium d
95	18	37.5	18	8	O19969	O19969 gossypium a
96	18	37.5	18	10	Q9S8Y9	Q9s8y9 poa pratens
97	17	35.4	8	8	Q34909	Q34909 locusta mig
98	17	35.4	9	6	Q9TRU7	Q9tru7 bos taurus
99	17	35.4	10	11	Q8VHM9	Q8vhm9 mus musculu
100	17	35.4	12	10	P82329	P82329 pisum sativ

#### ALIGNMENTS

##### RESULT 1

Q9NSF0

ID Q9NSF0 PRELIMINARY; PRT; 18 AA.

AC Q9NSF0;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE MESP1 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carim L., Estivill X., Escarceller M., Sumoy L.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,  
 RA Lehrach H., Poustka A., Lundberg J.;  
 RT "The European IMAGE consortium for integrated Molecular analysis of  
 RT human gene transcripts.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AL357535; CAB93427.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 2196 MW; 0ACBE7DA3E2849F0 CRC64;

Query Match 54.2%; Score 26; DB 4; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 :|::|||  
 Db 1 LETWMPLSP 9

## RESULT 2

### Q9TWL5

ID Q9TWL5 PRELIMINARY; PRT; 18 AA.  
 AC Q9TWL5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE 24 kDa chymotrypsin-like enzyme (Fragment).  
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Lucilia.  
 OX NCBI\_TaxID=7375;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95219141; PubMed=7704304;  
 RA Casu R.E., Pearson R.D., Jarmey J.M., Cadogan L.C., Riding G.A.,  
 RA Tellam R.L.;  
 RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,  
 RT enzymatic specificity and amino acid sequence deduced from mRNA.";  
 RL Insect Mol. Biol. 3:201-211(1994).  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 SQ SEQUENCE 18 AA; 2002 MW; AC29200B9B184300 CRC64;

Query Match 54.2%; Score 26; DB 5; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
 |:| |||

Db 6 EAYPGLFP 13

RESULT 3

Q9URC6

ID Q9URC6 PRELIMINARY; PRT; 17 AA.  
AC Q9URC6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Lipid-binding protein (Fragment).  
OS *Saccharomyces cerevisiae* (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; *Saccharomyces*.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91353077; PubMed=1882548;  
RA Creutz C.E., Snyder S.L., Kambouris N.G.;  
RT "Calcium-dependent secretory vesicle-binding and lipid-binding  
RT proteins of *Saccharomyces cerevisiae*."  
RL Yeast 7:229-244(1991).  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1959 MW; C2EB6543287744D2 CRC64;

Query Match 52.1%; Score 25; DB 3; Length 17;  
Best Local Similarity 57.1%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ESYVPLF 8  
: ||| |  
Db 2 QDYVPAF 8

RESULT 4

Q8RKN0

ID Q8RKN0 PRELIMINARY; PRT; 15 AA.  
AC Q8RKN0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative transposase ORF1005 (Fragment).  
GN ORF1005.  
OS *Escherichia coli*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Escherichia*.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=743-D;  
RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,  
RA Prats G.;  
RT "A novel complex *sul1*-type integron in *Escherichia coli* carrying the  
RT *bla*(CTX-M-9) gene."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY092058; AAM15719.1; -.

FT NON\_TER 1 1  
SQ SEQUENCE 15 AA; 1751 MW; 2D706E3A12001249 CRC64;

Query Match 50.0%; Score 24; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 6.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VESYVPL 7  
:| |:  
Db 6 IEGYLPV 12

#### RESULT 5

O82407

ID O82407 PRELIMINARY; PRT; 16 AA.  
AC O82407;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
GN ADH.  
OS *Fragaria viridis* (Wild strawberry).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Rosales; Rosaceae; Rosoideae; *Fragaria*.  
OX NCBI\_TaxID=64942;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FRA 341;  
RA Yu H., Davis T.M.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF000220; AAC36547.1; -.  
DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.  
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
KW Oxidoreductase.  
FT NON\_TER 1 1  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 50.0%; Score 24; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
| | | |  
Db 4 PLFP 7

#### RESULT 6

O82404

ID O82404 PRELIMINARY; PRT; 16 AA.  
AC O82404;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
 GN ADH.  
 OS *Fragaria nilgerrensis*.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Rosoideae; *Fragaria*.  
 OX NCBI\_TaxID=64941;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berlin 1;  
 RA Yu H., Davis T.M.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF000217; AAC36544.1; -.  
 DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
 DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.  
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 KW Oxidoreductase.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 50.0%; Score 24; DB 10; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 ||||  
 Db 4 PLFP 7

# RESULT 7

O82406

ID O82406 PRELIMINARY; PRT; 16 AA.  
 AC O82406;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
 GN ADH.  
 OS *Fragaria moschata*.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Rosoideae; *Fragaria*.  
 OX NCBI\_TaxID=64940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRA 157;  
 RA Yu H., Davis T.M.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF000219; AAC36546.1; -.  
 DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
 DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.  
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 KW Oxidoreductase.  
 FT NON\_TER 1 1

FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 50.0%; Score 24; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|  
Db 4 PLFP 7

RESULT 8

O82402

ID O82402 PRELIMINARY; PRT; 16 AA.  
AC O82402;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
GN ADH.  
OS Fragaria nubicola.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
OX NCBI\_TaxID=60188;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FRA520;  
RA Yu H., Davis T.M.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF000213; AAC36540.1; -.  
DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.  
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
KW Oxidoreductase.  
FT NON\_TER 1 1  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 50.0%; Score 24; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
|  
Db 4 PLFP 7

RESULT 9

O82403

ID O82403 PRELIMINARY; PRT; 16 AA.  
AC O82403;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
 GN ADH.  
 OS *Fragaria vesca* (Woodland strawberry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Rosoideae; *Fragaria*.  
 OX NCBI\_TaxID=57918;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Pawtuckaway;  
 RA Yu H., Davis T.M.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF000215; AAC36542.1; -.  
 DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
 DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.  
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 KW Oxidoreductase.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1666 MW; CEF73B5B28A4CA87 CRC64;

Query Match 50.0%; Score 24; DB 10; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 ||||  
 Db 4 PLFP 7

# RESULT 10

O82781

ID O82781 PRELIMINARY; PRT; 16 AA.  
 AC O82781;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Alcohol dehydrogenase (EC 1.1.1.1) (Aldehyde reductase) (Fragment).  
 GN ADH.  
 OS *Fragaria vesca* (Woodland strawberry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Rosoideae; *Fragaria*.  
 OX NCBI\_TaxID=57918;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YELLOW WONDER, and BARON SOLEMACHER;  
 RA Yu H., Davis T.M.;  
 RT "Genetic relationships among *Fragaria* species based on RAPDs and an  
 RT alcohol dehydrogenase (ADH) gene."  
 RL Genome 0:0-0(1997).  
 CC -!- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +  
 CC NADH.  
 CC -!- COFACTOR: ZINC OR IRON.  
 DR EMBL; AF000216; AAC36543.1; -.  
 DR EMBL; AF000214; AAC36541.1; -.



DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
 DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.  
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 KW Oxidoreductase.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 50.0%; Score 24; DB 10; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 ||||  
 Db 4 PLFP 7

# RESULT 11

O82405

ID O82405 PRELIMINARY; PRT; 16 AA.  
 AC O82405;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
 GN ADH.  
 OS Fragaria iinumae.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
 OX NCBI\_TaxID=64939;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRA 377;  
 RA Yu H., Davis T.M.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF000218; AAC36545.1; -.  
 DR GO; GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
 DR GO; GO:0004023; F:alcohol dehydrogenase activity, metal ion-i. . .; IEA.  
 DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 KW Oxidoreductase.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 50.0%; Score 24; DB 10; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 ||||  
 Db 4 PLFP 7

# RESULT 12

Q9T2U1

ID Q9T2U1 PRELIMINARY; PRT; 13 AA.  
AC Q9T2U1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE NADH:ubiquinone oxidoreductase (Complex I) iron-sulfur protein  
DE fraction 20 kDa polypeptide peptide T-9 (Fragment).  
OS Bos taurus (Bovine).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92138662; PubMed=1778979;  
RA Masui R., Wakabayashi S., Matsubara H., Hatefi Y.;  
RT "The amino acid sequence of the 9 kDa polypeptide and partial amino  
RT acid sequence of the 20 kDa polypeptide of mitochondrial  
RT NADH:ubiquinone oxidoreductase.";  
RL J. Biochem. 110:575-582(1991).  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1369 MW; 0E61A5EAB35FDB50 CRC64;

Query Match 47.9%; Score 23; DB 8; Length 13;  
Best Local Similarity 55.6%; Pred. No. 9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
|: ||| |  
Db 4 VDIYVPGCP 12

RESULT 13

Q52135

ID Q52135 PRELIMINARY; PRT; 15 AA.  
AC Q52135;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE (From E.faecalis) sex pheromone inhibitor (iAD1) determinant.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OG Plasmid pAD1.  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91261999; PubMed=2128961;  
RA Clewell D.B., Pontius L.T., An F.Y., Ike Y., Suzuki A., Nakayama J.;  
RT "Nucleotide sequence of the sex pheromone inhibitor (iAD1) determinant  
RT of Enterococcus faecalis conjugative plasmid pAD1.";  
RL Plasmid 24:156-161(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92250408; PubMed=1315730;

RA Pontius L.T., Clewell D.B.;  
 RT "Conjugative transfer of Enterococcus faecalis plasmid pAD1:  
 RT nucleotide sequence and transcriptional fusion analysis of a region  
 RT involved in positive regulation."  
 RL J. Bacteriol. 174:3152-3160(1992).  
 DR EMBL; M62888; AAA98040.1; -.  
 DR PIR; B41868; B41868.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 SQ SEQUENCE 15 AA; 1874 MW; 0D9D07E3079E3559 CRC64;

Query Match 47.9%; Score 23; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VESYVPLF 8  
 | |:  
 Db 4 VHVYIPRF 11

#### RESULT 14

Q9UCL5

ID Q9UCL5 PRELIMINARY; PRT; 18 AA.  
 AC Q9UCL5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Insulin-like growth factor binding protein 22 kDa form (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93091816; PubMed=1726837;  
 RA Roghani M., Segovia B., Whitechurch O., Binoux M.;  
 RT "Purification from human cerebrospinal fluid of insulin-like growth  
 RT factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered  
 RT form of IGFBP-3 and a new IGFBP species."  
 RL Growth Regul. 1:125-130(1991).  
 DR PIR; A54651; A54651.  
 SQ SEQUENCE 18 AA; 1948 MW; AC3F4170E95081E3 CRC64;

Query Match 47.9%; Score 23; DB 4; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
 :|:  
 Db 1 DSFVPXEP 8

#### RESULT 15

Q9S8V7

ID Q9S8V7 PRELIMINARY; PRT; 15 AA.  
 AC Q9S8V7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE High-molecular-weight glutenin subunit (Fragment).  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93003354; PubMed=1390908;  
 RA Tao H.P., Adalsteins A.E., Kasarda D.D.;  
 RT "Intermolecular disulfide bonds link specific high-molecular-weight  
 RT glutenin subunits in wheat endosperm."  
 RL Biochim. Biophys. Acta 1159:13-21(1992).  
 SQ SEQUENCE 15 AA; 1559 MW; CD1A6F573C945AFD CRC64;

Query Match 45.8%; Score 22; DB 10; Length 15;  
 Best Local Similarity 37.5%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
 : | | : |  
 Db 8 QGYYPISP 15

# RESULT 16

Q69353

ID Q69353 PRELIMINARY; PRT; 15 AA.  
 AC Q69353;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE HSV-2 (333) N terminus of 17.8 kDa protein gene (0.642 mu)  
 DE (Fragment).  
 OS Herpes simplex virus (type 2).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10310;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85033906; PubMed=6092683;  
 RA Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,  
 RA Wagner E.K.;  
 RT "Herpes simplex virus types 1 and 2 homology in the region between  
 RT 0.58 and 0.68 map units."  
 RL J. Virol. 52:615-623(1984).  
 DR EMBL; K03360; AAA45840.1; -.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1603 MW; 20B04D60BA4507FE CRC64;

Query Match 45.8%; Score 22; DB 12; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
 : | | |

## RESULT 17

Q32704

ID Q32704 PRELIMINARY; PRT; 11 AA.  
 AC Q32704;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE NdhE protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bright yellow 4; TISSUE=Leaf;  
 RX MEDLINE=88210537; PubMed=3329576;  
 RA Hayashida N., Matsubayashi T., Shinozaki K., Sugiura M., Inoue K.,  
 RA Hiyama T.;  
 RT "The gene for the 9kd polypeptide, a possible apoprotein for the iron-  
 RT sulfur centers A and B of the photosystem I complex in tobacco  
 RT chloroplastDNA.";  
 RL Curr. Genet. 12:247-250(1987).  
 DR EMBL; X05881; CAA29303.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1338 MW; 008165EE304776CB CRC64;

Query Match 43.8%; Score 21; DB 8; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPL 7  
 : || |:  
 Db 1 INSYQPI 7

## RESULT 18

Q83139

ID Q83139 PRELIMINARY; PRT; 12 AA.  
 AC Q83139;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (Strain CV17) genomic RNA-gamma, 5' leader.  
 OS Barley stripe mosaic virus (BSMV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.  
 OX NCBI\_TaxID=12327;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV17;  
 RX MEDLINE=91062385; PubMed=2247462;

RA Petty I.T., Edwards M.C., Jackson A.O.;  
RT "Systemic movement of an RNA plant virus determined by a point  
RT substitution in a 5' leader sequence."  
RL Proc. Natl. Acad. Sci. U.S.A. 87:8894-8897(1990).  
DR EMBL; M38633; AAA75527.1; -.  
SQ SEQUENCE 12 AA; 1416 MW; 36A281207BC05047 CRC64;

Query Match 43.8%; Score 21; DB 12; Length 12;  
Best Local Similarity 60.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7  
||:|:  
Db 2 SYMPI 6

#### RESULT 19

P82881

ID P82881 PRELIMINARY; PRT; 13 AA.  
AC P82881;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Temporin-1CB.  
OS Rana clamitans (green frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=145282;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin;  
RX MEDLINE=20283865; PubMed=10822101;  
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;  
RT "Purification and characterization of antimicrobial peptides from the  
RT skin of the North American green frog Rana clamitans."  
RL Peptides 21:469-476(2000).  
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM  
CC S.AUREUS.  
CC -!- SUBCELLULAR LOCATION: SECRETED.  
CC -!- MASS SPECTROMETRY: MW=1430.0; MW\_ERR=0.02; METHOD=ELECTROSPRAY.  
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN  
CC FAMILY.  
DR GO; GO:0006805; P:xenobiotic metabolism; IEA.  
KW Antibiotic; Amidation.  
FT MOD\_RES 13 13 AMIDATION.  
SQ SEQUENCE 13 AA; 1432 MW; C4A71A765A8935BD CRC64;

Query Match 43.8%; Score 21; DB 13; Length 13;  
Best Local Similarity 60.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPLF 8  
::|||  
Db 1 FLPLF 5

#### RESULT 20

Q9BGG8

ID Q9BGG8 PRELIMINARY; PRT; 16 AA.  
AC Q9BGG8;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Thyroid hormone receptor alpha (Fragment).  
GN THRA1.  
OS Sorex araneus (Eurasian common shrew) (European shrew).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.  
OX NCBI\_TaxID=42254;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Larkin D., Serov O., Zhdanova N.;  
RT "Mapping of five genes from human chromosome 17 to chromosome hn of  
RT the common shrew (Sorex araneus).";  
RL Acta Theriol. (Warsz) 45:143-146(2000).  
DR EMBL; AF314827; AAK13419.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F52E2 CRC64;

Query Match 43.8%; Score 21; DB 6; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2.8e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLF 8  
| : |||  
Db 1 ELFPPLF 7

RESULT 21

O54894

ID O54894 PRELIMINARY; PRT; 16 AA.  
AC O54894;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Putative membrane-associated guanylate kinase 1 (Fragment).  
GN BAIAP1 OR GUKM1 OR MAGI-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57 Black/6 x CBA;  
RA Dobrosotskaya I., Guy R.K., James G.L.;  
RT "MAGI-1: A Membrane-Associated Guanylate Kinase with a Unique  
RT Arrangement of Protein-Protein Interaction Domains.";  
RL J. Biol. Chem. 0:0-0(1997).  
DR EMBL; AF027504; AAB91996.1; -.  
DR MGD; MGI:1203522; Baiap1.  
DR GO; GO:0016301; F:kinase activity; IEA.  
KW Kinase.

FT NON\_TER 1 1  
SQ SEQUENCE 16 AA; 1668 MW; E15005C746D95D6B CRC64;

Query Match 43.8%; Score 21; DB 11; Length 16;  
Best Local Similarity 60.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
:| |  
Db 8 IPSFP 12

RESULT 22

Q9HB76

ID Q9HB76 PRELIMINARY; PRT; 17 AA.  
AC Q9HB76;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Arginine vasopressin (Fragment).  
GN AVP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lin M.T., Wang N., Chen Y.C., Fang L., Wu Z.Y., Murong S.X.;  
RT "A GAG deletion within two consecutive GAG sequences in exon 2 of the  
RT arginine vasopressin gene in Chinese."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF272848; AAG16747.1; -.  
DR HSSP; P01180; 1NPO.  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1923 MW; 7EFD60BD634B6B15 CRC64;

Query Match 43.8%; Score 21; DB 4; Length 17;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVP 6  
|:|:|  
Db 9 ENYLP 13

RESULT 23

Q85UU5

ID Q85UU5 PRELIMINARY; PRT; 18 AA.  
AC Q85UU5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein ORF51 (Fragment).  
OS Anthoceros formosae (Hornwort).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Anthocerotophyta;



OC Anthocerotales; Anthocerotaceae; Anthoceros.  
 OX NCBI\_TaxID=48387;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kugita M., Yamamoto Y., Fujikawa T., Matsumoto T., Yoshinaga K.;  
 RT "RNA editing in hornwort chloroplasts makes more than half the genes  
 RT functional.";  
 RL Nucleic Acids Res. 31:2417-2423(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22415709; PubMed=12527781;  
 RA Kugita M., Kaneko A., Yamamoto Y., Takeya Y., Matsumoto T.,  
 RA Yoshinaga K.;  
 RT "The complete nucleotide sequence of the hornwort (Anthoceros  
 RT formosae) chloroplast genome: insight into the earliest land plants.";  
 RL Nucleic Acids Res. 31:716-721(2003).  
 DR EMBL; AB087431; BAC55431.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast; Hypothetical protein.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2213 MW; E1F3C1DFE836D35A CRC64;  
  
 Query Match 43.8%; Score 21; DB 8; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 4 YVPLF 8  
 | |||  
 Db 13 YHPLF 17

RESULT 24

Q41458  
 ID Q41458 PRELIMINARY; PRT; 18 AA.  
 AC Q41458;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE HMG-CoA reductase (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Kennebec; TISSUE=Anther;  
 RX MEDLINE=95306778; PubMed=7787174;  
 RA Bhattacharyya M.K., Paiva N.L., Dixon R.A., Korth K.L., Stermer B.A.;  
 RT "Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase  
 RT in potato.";  
 RL Plant Mol. Biol. 28:1-15(1995).  
 DR EMBL; L34830; AAC37437.1; -.  
 DR PIR; S56715; S56715.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2181 MW; FD17C510527AA68F CRC64;

Query Match 43.8%; Score 21; DB 10; Length 18;  
Best Local Similarity 75.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||:|  
Db 10 PLYP 13

RESULT 25

Q56972

ID Q56972 PRELIMINARY; PRT; 11 AA.  
AC Q56972;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE LcrKb protein (Fragment).  
GN LCRKB.  
OS Yersinia pestis.  
OG Plasmid Lcr.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=358;  
RX MEDLINE=92250432; PubMed=1577700;  
RA Rimpilaeinen M., Forsberg A., Wolf-Watz H.;  
RT "A novel protein, LcrQ, involved in the low-calcium response of  
RT Yersinia pseudotuberculosis shows extensive homology to YopH."  
RL J. Bacteriol. 174:3355-3363(1992).  
DR EMBL; X78303; CAA55113.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1377 MW; 0478BFECA1A04B54 CRC64;

Query Match 41.7%; Score 20; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 3e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPLF 8  
:|:|: |  
Db 2 MENYITSF 9

RESULT 26

O88175

ID O88175 PRELIMINARY; PRT; 15 AA.  
AC O88175;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Neural cell adhesion molecule (Fragment).  
GN NCAM1 OR NCAM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb-c; TISSUE=Liver;  
 RX MEDLINE=98250618; PubMed=9582442;  
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;  
 RT "A cis-acting regulatory element that affects the alternative splicing  
 RT of a muscle-specific exon in the mouse NCAM gene."  
 RL Biochim. Biophys. Acta 1397:305-315(1998).  
 DR EMBL; AB001873; BAA31274.1; -.  
 DR MGD; MGI:97281; Ncam1.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1481 MW; 41868EF6117732C2 CRC64;

Query Match 41.7%; Score 20; DB 11; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4.2e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
 ||| |  
 Db 9 VPLSP 13

#### RESULT 27

##### Q9WMG6

ID Q9WMG6 PRELIMINARY; PRT; 16 AA.  
 AC Q9WMG6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE 2 protein (Fragment).  
 GN 2.  
 OS Sigma virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Rhabdoviridae; unclassified Rhabdoviridae.  
 OX NCBI\_TaxID=11301;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212481; PubMed=8384742;  
 RA Teninges D., Bras F., Dezelee S.;  
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene  
 RT overlap."  
 RL Virology 193:1018-1023(1993).  
 DR EMBL; S57847; AAD40699.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 16 AA; 1904 MW; F96DBC468601967E CRC64;

Query Match 41.7%; Score 20; DB 12; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 | | : |  
 Db 9 YEPVLP 14

RESULT 28

Q9S8J8

ID Q9S8J8 PRELIMINARY; PRT; 9 AA.  
 AC Q9S8J8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE ORYZATENSIN=BIOACTIVE peptide.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95102521; PubMed=7804141;  
 RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;  
 RT "Isolation and characterization of oryzatensin: a novel bioactive  
 RT peptide with ileum-contracting and immunomodulating activities derived  
 RT from rice albumin.";  
 RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).  
 DR Gramene; Q9S8J8; -.  
 SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 39.6%; Score 19; DB 10; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 |::|  
 Db 3 PMYP 6

RESULT 29

Q96WW8

ID Q96WW8 PRELIMINARY; PRT; 13 AA.  
 AC Q96WW8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Lipase I (Fragment).  
 GN LIP1.  
 OS Geotrichum candidum (Oospora lactis).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Galactomyces.  
 OX NCBI\_TaxID=27317;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC34614;  
 RX MEDLINE=93380907; PubMed=8370674;  
 RA Nagao T., Shimada Y., Sugihara A., Tominaga Y.;  
 RT "Cloning and sequencing of two chromosomal lipase genes from  
 RT Geotrichum candidum.";  
 RL J. Biochem. 113:776-780(1993).  
 DR EMBL; S65082; AAB28107.1; -.  
 FT NON\_TER 1 1

SQ SEQUENCE 13 AA; 1385 MW; 7FFB77B4C851B5BB CRC64;

Query Match 39.6%; Score 19; DB 3; Length 13;  
Best Local Similarity 71.4%; Pred. No. 5.7e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPLF 8  
|| | ||  
Db 6 ESDVTLF 12

RESULT 30

Q9P2A2

ID Q9P2A2 PRELIMINARY; PRT; 14 AA.  
AC Q9P2A2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Truncated aldo-keto reductase (Fragment).  
GN TRUNCATED AKR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20138537; PubMed=10672042;  
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,  
RA Watanabe K., Ito S.;  
RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with  
RT three aldo-keto reductase genes."  
RL Genes Cells 5:111-125(2000).  
DR EMBL; AB037903; BAA92888.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 39.6%; Score 19; DB 4; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
||| |  
Db 5 VPLQP 9

RESULT 31

O70599

ID O70599 PRELIMINARY; PRT; 14 AA.  
AC O70599;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Thymidine kinase (EC 2.7.1.21) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Sauer M.;  
 RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.  
 DR EMBL; AJ006455; CAA07030.1; -.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0004797; F:thymidine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 KW Kinase; Transferase.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 39.6%; Score 19; DB 11; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
 :| ||  
 Db 10 LPSFP 14

#### RESULT 32

Q9NY39

ID Q9NY39 PRELIMINARY; PRT; 17 AA.  
 AC Q9NY39;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE CHI3L1 protein (Fragment).  
 GN CHI3L1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ammon C., Rehli M., Andreessen R., Krause S.W.;  
 RT "Alternative splicing of the human cartilage gp-39 gene generates  
 RT multiple mRNA transcripts encoding for at least four putative protein  
 RT isoforms with distinct carboxyl termini."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ251847; CAB76474.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 2099 MW; 086B9AA863393785 CRC64;

Query Match 39.6%; Score 19; DB 4; Length 17;  
 Best Local Similarity 33.3%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 ::| |  
 Db 10 FIPTLP 15

#### RESULT 33

Q7YAT7

ID Q7YAT7 PRELIMINARY; PRT; 17 AA.  
AC Q7YAT7;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ATP6 (Fragment).  
GN ATP6.  
OS Cooperia oncophora.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
OC Trichostrongyloidea; Cooperiidae; Cooperia.  
OX NCBI\_TaxID=27828;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA van der Veer M., de Vries E.;  
RT "SNP analysis of two populations of the parasitic nematode Cooperia  
RT oncophora.";  
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY291776; AAP45607.1; -.  
KW Mitochondrion.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 2155 MW; 0E2E1EBF3400CB58 CRC64;

Query Match 39.6%; Score 19; DB 8; Length 17;  
Best Local Similarity 40.0%; Pred. No. 7.5e+03;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
::||:  
Db 2 IQSYI 6

RESULT 34

Q7Y834

ID Q7Y834 PRELIMINARY; PRT; 17 AA.  
AC Q7Y834;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ATP6 (Fragment).  
GN ATP6.  
OS Cooperia oncophora.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
OC Trichostrongyloidea; Cooperiidae; Cooperia.  
OX NCBI\_TaxID=27828;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA van der Veer M., de Vries E.;  
RT "SNP analysis of two populations of the parasitic nematode Cooperia  
RT oncophora.";  
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY291699; AAP45527.1; -.  
DR EMBL; AY291700; AAP45528.1; -.  
DR EMBL; AY291701; AAP45529.1; -.  
DR EMBL; AY291702; AAP45530.1; -.

DR EMBL; AY291703; AAP45531.1; -.  
DR EMBL; AY291704; AAP45532.1; -.  
DR EMBL; AY291705; AAP45533.1; -.  
DR EMBL; AY291706; AAP45534.1; -.  
DR EMBL; AY291707; AAP45535.1; -.  
DR EMBL; AY291708; AAP45536.1; -.  
DR EMBL; AY291709; AAP45537.1; -.  
DR EMBL; AY291710; AAP45538.1; -.  
DR EMBL; AY291711; AAP45539.1; -.  
DR EMBL; AY291712; AAP45540.1; -.  
DR EMBL; AY291713; AAP45541.1; -.  
DR EMBL; AY291714; AAP45542.1; -.  
DR EMBL; AY291715; AAP45543.1; -.  
DR EMBL; AY291716; AAP45544.1; -.  
DR EMBL; AY291717; AAP45545.1; -.  
DR EMBL; AY291718; AAP45546.1; -.  
DR EMBL; AY291719; AAP45547.1; -.  
DR EMBL; AY291720; AAP45548.1; -.  
DR EMBL; AY291721; AAP45549.1; -.  
DR EMBL; AY291722; AAP45550.1; -.  
DR EMBL; AY291723; AAP45551.1; -.  
DR EMBL; AY291724; AAP45552.1; -.  
DR EMBL; AY291725; AAP45553.1; -.  
DR EMBL; AY291726; AAP45554.1; -.  
DR EMBL; AY291727; AAP45555.1; -.  
DR EMBL; AY291728; AAP45556.1; -.  
DR EMBL; AY291729; AAP45557.1; -.  
DR EMBL; AY291730; AAP45558.1; -.  
DR EMBL; AY291731; AAP45559.1; -.  
DR EMBL; AY291732; AAP45560.1; -.  
DR EMBL; AY291733; AAP45561.1; -.  
DR EMBL; AY291734; AAP45562.1; -.  
DR EMBL; AY291735; AAP45563.1; -.  
DR EMBL; AY291736; AAP45564.1; -.  
DR EMBL; AY291737; AAP45565.1; -.  
DR EMBL; AY291738; AAP45566.1; -.  
DR EMBL; AY291739; AAP45567.1; -.  
DR EMBL; AY291740; AAP45568.1; -.  
DR EMBL; AY291741; AAP45569.1; -.  
DR EMBL; AY291742; AAP45570.1; -.  
DR EMBL; AY291743; AAP45571.1; -.  
DR EMBL; AY291744; AAP45572.1; -.  
DR EMBL; AY291745; AAP45573.1; -.  
DR EMBL; AY291746; AAP45574.1; -.  
DR EMBL; AY291747; AAP45575.1; -.  
DR EMBL; AY291748; AAP45576.1; -.  
DR EMBL; AY291749; AAP45580.1; -.  
DR EMBL; AY291750; AAP45581.1; -.  
DR EMBL; AY291751; AAP45582.1; -.  
DR EMBL; AY291752; AAP45583.1; -.  
DR EMBL; AY291753; AAP45584.1; -.  
DR EMBL; AY291754; AAP45585.1; -.  
DR EMBL; AY291755; AAP45586.1; -.  
DR EMBL; AY291756; AAP45587.1; -.  
DR EMBL; AY291757; AAP45588.1; -.  
DR EMBL; AY291758; AAP45589.1; -.  
DR EMBL; AY291759; AAP45590.1; -.



DR EMBL; AY291760; AAP45591.1; -.  
 DR EMBL; AY291761; AAP45592.1; -.  
 DR EMBL; AY291762; AAP45593.1; -.  
 DR EMBL; AY291763; AAP45594.1; -.  
 DR EMBL; AY291764; AAP45595.1; -.  
 DR EMBL; AY291765; AAP45596.1; -.  
 DR EMBL; AY291766; AAP45597.1; -.  
 DR EMBL; AY291767; AAP45598.1; -.  
 DR EMBL; AY291768; AAP45599.1; -.  
 DR EMBL; AY291769; AAP45600.1; -.  
 DR EMBL; AY291770; AAP45601.1; -.  
 DR EMBL; AY291771; AAP45602.1; -.  
 DR EMBL; AY291772; AAP45603.1; -.  
 DR EMBL; AY291773; AAP45604.1; -.  
 DR EMBL; AY291774; AAP45605.1; -.  
 DR EMBL; AY291775; AAP45606.1; -.  
 DR EMBL; AY291777; AAP45608.1; -.  
 DR EMBL; AY291778; AAP45609.1; -.  
 DR EMBL; AY291779; AAP45610.1; -.  
 DR EMBL; AY291780; AAP45611.1; -.  
 DR EMBL; AY291781; AAP45612.1; -.  
 DR EMBL; AY291782; AAP45613.1; -.  
 DR EMBL; AY291783; AAP45614.1; -.  
 DR EMBL; AY291784; AAP45615.1; -.  
 DR EMBL; AY291785; AAP45616.1; -.  
 DR EMBL; AY291786; AAP45617.1; -.  
 DR EMBL; AY291787; AAP45618.1; -.  
 DR EMBL; AY291788; AAP45619.1; -.  
 DR EMBL; AY291789; AAP45620.1; -.  
 DR EMBL; AY291790; AAP45621.1; -.  
 DR EMBL; AY291791; AAP45622.1; -.  
 DR EMBL; AY291792; AAP45623.1; -.  
 DR EMBL; AY291793; AAP45624.1; -.  
 DR EMBL; AY291794; AAP45625.1; -.  
 DR EMBL; AY291795; AAP45626.1; -.  
 DR EMBL; AY291796; AAP45627.1; -.  
 DR EMBL; AY291797; AAP45628.1; -.  
 DR EMBL; AY291798; AAP45629.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 2183 MW; 0E3FEEBF3400CB58 CRC64;

Query Match 39.6%; Score 19; DB 8; Length 17;  
 Best Local Similarity 40.0%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
 :||:  
 Db 2 IQSYI 6

RESULT 35

Q9QVH7

ID Q9QVH7 PRELIMINARY; PRT; 17 AA.

AC Q9QVH7;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Alpha-2-macroglobulin (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92041742; PubMed=1718949;  
 RA Enjyoji K., Miyazaki K., Kato H.;  
 RT "Characterization of rat factors X and Xa: demonstration of factor Xa  
 RT in rat plasma.";  
 RL J. Biochem. 109:890-898(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1834 MW; 7E40E70214EF8202 CRC64;  
  
 Query Match 39.6%; Score 19; DB 11; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 7.5e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 Qy 4 YVPLFP 9  
 || ||  
 Db 7 YVVLVP 12

# RESULT 36

Q7YXH4

ID Q7YXH4 PRELIMINARY; PRT; 18 AA.  
 AC Q7YXH4;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Neuropeptide-like protein 16, isoform b.  
 GN NLP-16.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA Wilson R.;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Nelson J.;  
 RT "The sequence of C. elegans cosmid T13A10.";  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;

RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wilson R.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U56963; AAQ01524.1; -.  
 KW Neuropeptide.  
 SQ SEQUENCE 18 AA; 2047 MW; A1176979A6CFF773 CRC64;

Query Match 39.6%; Score 19; DB 5; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 8e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VPLFP 9  
 :| ||  
 Db 1 MPSFP 5

# RESULT 37

Q8ZSZ9

ID Q8ZSZ9 PRELIMINARY; PRT; 18 AA.  
 AC Q8ZSZ9;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein PAE3501a.  
 GN PAE3501A.  
 OS Pyrobaculum aerophilum.  
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
 OC Thermoproteaceae; Pyrobaculum.  
 OX NCBI\_TaxID=13773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;  
 RX MEDLINE=21664397; PubMed=11792869;  
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
 RA Miller J.H.;  
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
 RT aerophilum.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
 DR EMBL; AE009934; AAL64964.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 18 AA; 2262 MW; BCFF4D6923A98943 CRC64;

Query Match 39.6%; Score 19; DB 17; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 8e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYV 5  
 |||:  
 Db 3 ESYI 6

# RESULT 38

Q9P8E5

ID Q9P8E5 PRELIMINARY; PRT; 9 AA.

AC Q9P8E5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE HIS4 protein (Fragment).  
 GN HIS4.  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL-Y1140;  
 RX MEDLINE=99448382; PubMed=10518937;  
 RA Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;  
 RT "Kluyveromyces lacxtis HIS4 transcriptional regulation: similarities  
 RT and differences to Saccharomyces cerevisiae HIS4 gene."  
 RL FEBS Lett. 458:72-76(1999).  
 DR EMBL; AJ238494; CAB87125.1; -.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 37.5%; Score 18; DB 3; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLF 8  
 ||:  
 Db 5 VPVF 8

RESULT 39  
 Q88612

ID Q88612 PRELIMINARY; PRT; 9 AA.  
 AC Q88612;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Structural polyprotein (Fragment).  
 OS Middelburg virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus.  
 OX NCBI\_TaxID=11023;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83039346; PubMed=6291034;  
 RA Ou J.H., Rice C.M., Dalgarno L., Strauss E.G., Strauss J.H.;  
 RT "Sequence studies of several alphavirus genomic RNAs in the region  
 RT containing the start of the subgenomic RNA."  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:5235-5239(1982).  
 DR EMBL; J02246; AAA96655.1; -.  
 KW Polyprotein.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1114 MW; 00E8B6C1B7604B54 CRC64;

Query Match 37.5%; Score 18; DB 12; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6  
:|:|  
Db 2 NYIP 5

RESULT 40

Q9TRY4

ID Q9TRY4 PRELIMINARY; PRT; 12 AA.  
AC Q9TRY4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).  
OS Sus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9826;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92049376; PubMed=1719383;  
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;  
RT "Isolation and molecular cloning of insulin-like growth factor-binding  
RT protein-6."  
RL Mol. Endocrinol. 5:938-948(1991).  
FT NON\_TER 1 1  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1317 MW; 4DAAABE6CC72DB57 CRC64;

Query Match 37.5%; Score 18; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
|||  
Db 6 YVP 8

RESULT 41

Q63047

ID Q63047 PRELIMINARY; PRT; 13 AA.  
AC Q63047;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE AMP deaminase (Fragment).  
GN AMPD1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Soleus muscle;  
RX MEDLINE=90377216; PubMed=2398891;  
RA Mineo I., Clarke P.R.H., Sabina R.L., Holmes E.W.;

RT "A novel pathway for alternative splicing: Identification of an RNA  
RT intermediate that generates an alternative 5' splice donor site not  
RT present in the primary transcript of AMPD1.";  
RL Mol. Cell. Biol. 10:5271-5278(1990).  
DR EMBL; M58689; AAA40727.1; -.  
DR PIR; I77387; I77387.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1524 MW; 526C5A93EF6201A7 CRC64;

Query Match 37.5%; Score 18; DB 11; Length 13;  
Best Local Similarity 75.0%; Pred. No. 8.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLF 8  
:|  
Db 1 MPLF 4

# RESULT 42

## Q9PVA0

ID Q9PVA0 PRELIMINARY; PRT; 13 AA.  
AC Q9PVA0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Colisa lalia (dwarf gourami).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Anabantoidei; Belontiidae; Colisa.  
OX NCBI\_TaxID=50373;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aGouramy;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134625; AAD54110.1; -.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
||:  
Db 9 VETYL 13

RESULT 43

Q9PVB1

ID Q9PVB1 PRELIMINARY; PRT; 13 AA.  
 AC Q9PVB1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Growth hormone (Fragment).  
 GN GH.  
 OS Dendrochirus zebra (Zebra turkeyfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;  
 OC Scorpaenoidei; Scorpaenidae; Dendrochirus.  
 OX NCBI\_TaxID=94308;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gh4alionfish;  
 RX MEDLINE=99398697; PubMed=10468597;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate  
 RT evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF134614; AAD54099.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; hormone; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
 |||:  
 Db 9 VETYL 13

RESULT 44

Q9PV95

ID Q9PV95 PRELIMINARY; PRT; 13 AA.  
 AC Q9PV95;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Growth hormone (Fragment).  
 GN GH.  
 OS Mola mola (ocean sunfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Molidae; Mola.

OX NCBI\_TaxID=94237;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gh4aSunfish;  
 RX MEDLINE=99398697; PubMed=10468597;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate  
 RT evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF134630; AAD54115.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; hormone; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
 ||:|:  
 Db 9 VETYL 13

#### RESULT 45

##### Q9PVA7

ID Q9PVA7 PRELIMINARY; PRT; 13 AA.  
 AC Q9PVA7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Growth hormone (Fragment).  
 GN GH.  
 OS Dissostichus mawsoni (Antarctic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
 OC Notothenioidae; Nototheniidae; Dissostichus.  
 OX NCBI\_TaxID=36200;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gh4atooth;  
 RX MEDLINE=99398697; PubMed=10468597;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate  
 RT evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF134618; AAD54103.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; hormone; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13



SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
||:|:  
Db 9 VETYL 13

RESULT 46

Q9PVB3

ID Q9PVB3 PRELIMINARY; PRT; 13 AA.  
AC Q9PVB3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Hippocampus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;  
OC Syngnathidae; Hippocampus.  
OX NCBI\_TaxID=72047;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aseahorse;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134612; AAD54097.1; -.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
||:|:  
Db 9 VETYL 13

RESULT 47

Q9PV98

ID Q9PV98 PRELIMINARY; PRT; 13 AA.  
AC Q9PV98;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Growth hormone (Fragment).  
 GN GH.  
 OS Psettodes sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Psettodidae; Psettodidae; Psettodes.  
 OX NCBI\_TaxID=94241;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gh4aFlatfish;  
 RX MEDLINE=99398697; PubMed=10468597;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate  
 evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF134627; AAD54112.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; hormone; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
 ||:|:  
 Db 9 VETYL 13

#### RESULT 48

Q9PV97

ID Q9PV97 PRELIMINARY; PRT; 13 AA.  
 AC Q9PV97;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Growth hormone (Fragment).  
 GN GH.  
 OS Balistes sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Balistidae; Balistes.  
 OX NCBI\_TaxID=94230;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gh4aTrigger;  
 RX MEDLINE=99398697; PubMed=10468597;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate

RT evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF134628; AAD54113.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; hormone; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
 ||:|:  
 Db 9 VETYL 13

# RESULT 49

Q9PVB2

ID Q9PVB2 PRELIMINARY; PRT; 13 AA.  
 AC Q9PVB2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Growth hormone (Fragment).  
 GN GH.  
 OS Mastacembelus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;  
 OC Mastacembelidae; Mastacembelus.  
 OX NCBI\_TaxID=94235;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gh4aMasta;  
 RX MEDLINE=99398697; PubMed=10468597;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate  
 RT evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF134613; AAD54098.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; hormone; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 37.5%; Score 18; DB 13; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5

Db                    ||:|:  
9 VETYL 13

RESULT 50

Q9PVA2

ID    Q9PVA2            PRELIMINARY;            PRT;        13 AA.  
AC    Q9PVA2;  
DT    01-MAY-2000 (TrEMBLrel. 13, Created)  
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE    Growth hormone (Fragment).  
GN    GH.  
OS    Thunnus sp.  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC    Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC    Scombridae; Thunnus.  
OX    NCBI\_TaxID=8239;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RC    STRAIN=Gh4aTuna;  
RX    MEDLINE=99398697; PubMed=10468597;  
RA    Venkatesh B., Ning Y., Brenner S.;  
RT    "Late changes in spliceosomal introns define clades in vertebrate  
RT    evolution.";  
RL    Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR    EMBL; AF134623; AAD54108.1; -.  
DR    GO; GO:0005576; C:extracellular; IEA.  
DR    GO; GO:0005179; F:hormone activity; IEA.  
DR    InterPro; IPR001400; Somatotropin.  
DR    Pfam; PF00103; hormone; 1.  
FT    NON\_TER            1            1  
FT    NON\_TER            13           13  
SQ    SEQUENCE    13 AA;   1642 MW;   AA37BE5A8E4C31E6 CRC64;

Query Match                    37.5%;    Score 18;    DB 13;    Length 13;  
Best Local Similarity    60.0%;    Pred. No. 8.9e+03;  
Matches    3;    Conservative    2;    Mismatches    0;    Indels    0;    Gaps    0;

Qy                    1 VESYV 5  
                      ||:|:  
Db                    9 VETYL 13

Search completed: July 4, 2004, 04:45:43  
Job time : 17.3134 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 3.08955 Seconds  
(without alignments)  
151.683 Million cell updates/sec

Title: US-09-641-802-31  
Perfect score: 48  
Sequence: 1 VESYVPLFP 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	25	52.1	18	1	AGI_EUPCH	P33888	euphorbia c
2	24	50.0	9	1	UPA3_HUMAN	P30089	homo sapien
3	21	43.8	15	1	CXA2_CONAL	P56640	conus aulic
4	21	43.8	15	1	PH2_PERAM	P82695	periplaneta
5	21	43.8	16	1	CXA1_CONAL	P56639	conus aulic
6	21	43.8	16	1	CXA3_CONAL	P56641	conus aulic
7	21	43.8	17	1	PH3_PERAM	P82696	periplaneta
8	20	41.7	12	1	RF1_CONSP	P58805	conus spuri
9	20	41.7	15	1	SAL1_ONCMY	P81369	oncorhynchu
10	19	39.6	13	1	TY13_PHYRO	P04096	phyllomedus
11	19	39.6	14	1	ECDC_LYMDI	P80940	lymantria d
12	19	39.6	15	1	COXJ_THUOB	P80979	thunnus obe
13	18	37.5	8	1	UPA1_HUMAN	P30087	homo sapien
14	18	37.5	14	1	PPK6_PERAM	P82693	periplaneta
15	18	37.5	15	1	ECDA_LYMDI	P80938	lymantria d
16	18	37.5	15	1	LPF_ECOLI	P03057	escherichia
17	18	37.5	15	1	UC17_MAIZE	P80623	zea mays (m

18	18	37.5	15	1	UC30_MAIZE	P80636	zea mays (m
19	18	37.5	17	1	RM35_YEAST	P36530	saccharomyc
20	18	37.5	18	1	FIBB_ANAPL	P12802	anas platyr
21	17	35.4	9	1	UPA7_HUMAN	P30093	homo sapien
22	17	35.4	12	1	TM2A_METMA	P80652	methanosarc
23	17	35.4	17	1	APID_BOMPA	P81464	bombus pasc
24	16	33.3	10	1	LPK2_LOCFI	P41488	locusta mig
25	16	33.3	10	1	TKNB_ONCFI	P28500	oncorhynchu
26	16	33.3	11	1	TKND_RANCA	P22691	rana catesb
27	16	33.3	12	1	GRAR_RANRU	P40754	rana rugosa
28	16	33.3	13	1	ADFB_TENMO	P83109	tenebrio mo
29	16	33.3	13	1	YPE2_LACLC	P42021	lactococcus
30	16	33.3	16	1	HP29_SARPE	P29184	sarcophaga
31	16	33.3	16	1	VPR_HV1S3	P19555	human immun
32	15.5	32.3	18	1	AHD2_TETPY	P35430	tetrahymena
33	15	31.2	8	1	ALL6_CYPDO	P82157	cydia pomon
34	15	31.2	8	1	PPK3_PERAM	P82618	periplaneta
35	15	31.2	9	1	LMT3_LOCFI	P41489	locusta mig
36	15	31.2	10	1	RT02_BOVIN	P82923	bos taurus
37	15	31.2	10	1	TKNB_CHICK	P19851	gallus gall
38	15	31.2	10	1	TKNB_RANRI	P29135	rana ridibu
39	15	31.2	10	1	UPA8_HUMAN	P30094	homo sapien
40	15	31.2	12	1	NUDM_CANFA	P54713	canis famil
41	15	31.2	13	1	CRBL_VESCR	P01518	vespa crabr
42	15	31.2	13	1	HPB9_RANES	P32416	rana escule
43	15	31.2	13	1	PSAJ_PEA	P17229	pisum sativ
44	15	31.2	13	1	TEMA_RANTE	P56917	rana tempor
45	15	31.2	13	1	TEMF_RANTE	P56921	rana tempor
46	15	31.2	14	1	CRBL_VESOR	P17236	vespa orien
47	15	31.2	16	1	LPK1_LOCFI	P20404	locusta mig
48	15	31.2	16	1	MLB_SQUAC	P01207	squalus aca
49	15	31.2	18	1	ALL2_CYPDO	P82153	cydia pomon
50	15	31.2	18	1	CPAX_BOVIN	P22779	bos taurus
51	15	31.2	18	1	FMF1_ECOLI	P20860	escherichia
52	14	29.2	7	1	TPFY_PACDA	P83455	pachymedusa
53	14	29.2	7	1	TY51_LITRU	P82065	litoria rub
54	14	29.2	8	1	LPK_LEUMA	P13049	leucophaea
55	14	29.2	9	1	COXE_THUOB	P80975	thunnus obe
56	14	29.2	11	1	PKC1_CARMO	P82684	carausius m
57	14	29.2	11	1	TIN4_HOPTI	P82654	hoplobatrac
58	14	29.2	12	1	TIN2_HOPTI	P82652	hoplobatrac
59	14	29.2	12	1	TIN3_HOPTI	P82653	hoplobatrac
60	14	29.2	13	1	IDHA_CANFA	P54836	canis famil
61	14	29.2	14	1	CAL1_CALGI	P20728	calotropis
62	14	29.2	14	1	HY14_PIG	P01155	sus scrofa
63	14	29.2	14	1	MCRZ_METTM	P58816	methanobact
64	14	29.2	14	1	PH1_PRUSE	P29263	prunus sero
65	14	29.2	15	1	CX3A_CONQU	P58841	conus querc
66	14	29.2	15	1	CX3B_CONQU	P58842	conus querc
67	14	29.2	15	1	LEC1_PSOSC	P22582	psophocarpu
68	14	29.2	15	1	LEC3_AXIPO	P28588	axinella po
69	14	29.2	15	1	PH3_PRUSE	P29265	prunus sero
70	14	29.2	15	1	PSAO_CUCSA	P42052	cucumis sat
71	14	29.2	15	1	UC08_MAIZE	P80614	zea mays (m
72	14	29.2	15	1	UC29_MAIZE	P80635	zea mays (m
73	14	29.2	15	1	URE1_MORMO	P17337	morganella
74	14	29.2	16	1	PGTL_PELAC	P80563	pelobacter

75	14	29.2	16	1	PH2_PRUSE	P29264	prunus sero
76	14	29.2	16	1	SSIT_STRMB	P83544	streptomyce
77	14	29.2	17	1	ALYS_MYCPH	P81528	mycobacteri
78	14	29.2	17	1	PH4_PERAM	P82697	periplaneta
79	14	29.2	17	1	TPIS_PINPS	P81666	pinus pinas
80	13	27.1	7	1	ALL2_CARMA	P81805	carcinus ma
81	13	27.1	8	1	AKH_MELML	P25423	melolontha
82	13	27.1	9	1	PGLR_DIAAB	P81179	diaprepes a
83	13	27.1	9	1	PPK1_PERAM	P82691	periplaneta
84	13	27.1	9	1	SAMP_MUSCA	P19095	mustelus ca
85	13	27.1	10	1	PVK_LOCFI	P83382	locusta mig
86	13	27.1	10	1	Q2OB_COMTE	P80465	comamonas t
87	13	27.1	10	1	SLAP_BACTG	P49325	bacillus th
88	13	27.1	10	1	TMOF_AEDAE	P19425	aedes aegyp
89	13	27.1	11	1	MORN_HUMAN	P01163	homo sapien
90	13	27.1	13	1	ACT7_SOYBN	P15987	glycine max
91	13	27.1	13	1	BP37_LEUMA	P81754	leucophaea
92	13	27.1	13	1	CRBL_VESAN	P17233	vespa anali
93	13	27.1	13	1	CRBL_VESLE	P17235	vespula lew
94	13	27.1	13	1	CRBL_VESMA	P17232	vespa manda
95	13	27.1	13	1	CRBL_VESTR	P17231	vespa tropi
96	13	27.1	13	1	CRBL_VESXA	P17234	vespa xanth
97	13	27.1	13	1	LMT4_LOCFI	P41490	locusta mig
98	13	27.1	13	1	MP1_MICOC	P81532	microplitis
99	13	27.1	14	1	ATP6_SPIOL	P80086	spinacia ol
100	13	27.1	14	1	EFTU_CANFA	P54835	canis famil

#### ALIGNMENTS

#### RESULT 1

#### AGI\_EUPCH

ID AGI\_EUPCH STANDARD; PRT; 18 AA.

AC P33888;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Lectin (Fragment).

OS Euphorbia characias (Spurge).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae; Euphorbieae;

OC Euphorbia.

OX NCBI\_TaxID=3991;

RN [1]

RP SEQUENCE.

RC TISSUE=Latex;

RX MEDLINE=93357266; PubMed=8353129;

RA Stirpe F., Licastro F., Morini M.C., Parente A., Savino G.,

RA Abbondanza A., Bolognesi A., Falasca A.I., Rossi C.A.;

RT "Purification and partial characterization of a mitogenic lectin from

RT the latex of Euphorbia marginata.";

RL Biochim. Biophys. Acta 1158:33-39(1993).

CC -!- FUNCTION: Lectin that binds galactose, galactose-containing sugars

CC and gentiobiose. It is strongly mitogenic for human T lymphocytes.

CC -!- SUBUNIT: Homodimer.

CC -!- PTM: N-glycosylated.  
CC -!- SIMILARITY: TO E.MARGINATA LECTIN.  
DR PIR; S36121; S36121.  
KW Lectin.  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1923 MW; C6F6A1A7B2AB124F CRC64;

Query Match 52.1%; Score 25; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 74;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVPL 7  
||| |:  
Db 2 ESYTPI 7

#### RESULT 2

##### UPA3\_HUMAN

ID UPA3\_HUMAN STANDARD; PRT; 9 AA.  
AC P30089;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 4.6, its MW is: 46 kDa.  
DR SWISS-2DPAGE; P30089; HUMAN.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 50.0%; Score 24; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
||||  
Db 2 PLFP 5

#### RESULT 3

##### CXA2\_CONAL

ID CXA2\_CONAL STANDARD; PRT; 15 AA.  
AC P56640;



DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-conotoxin AuIB.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RA Olivera B.M., McIntosh J.M.;  
 RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic  
 RT acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 RN [2]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=20187585; PubMed=10722709;  
 RA Cho J.H., Mok K.H., Olivera B.M., McIntosh J.M., Park K.H., Han K.H.;  
 RT "Nuclear magnetic resonance solution conformation of alpha-conotoxin  
 RT AuIB, an alpha(3)beta(4) subtype-selective neuronal nicotinic  
 RT acetylcholine receptor antagonist.";  
 RL J. Biol. Chem. 275:8680-8685(2000).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=22359066; PubMed=12376538;  
 RA Dutton J.L., Bansal P.S., Hogg R.C., Adams D.J., Alewood P.F.,  
 RA Craik D.J.;  
 RT "A new level of conotoxin diversity, a non-native disulfide bond  
 RT connectivity in alpha-conotoxin AuIB reduces structural definition  
 RT but increases biological activity.";  
 RL J. Biol. Chem. 277:48849-48857(2002).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide blocks mammalian nicotinic  
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PDB; 1DG2; 23-MAY-00.  
 DR PDB; 1MXN; 30-DEC-02.  
 DR PDB; 1MXP; 30-DEC-02.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
 FT DISULFID 2 8  
 FT DISULFID 3 15  
 FT MOD\_RES 15 15 AMIDATION.  
 SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;

Query Match 43.8%; Score 21; DB 1; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy            3 SYVPLF 8  
              || | |  
Db            4 SYPPCF 9

RESULT 4

PH2\_PERAM

ID PH2\_PERAM            STANDARD;            PRT;        15 AA.  
AC P82695;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Peptide hormone 2 (Pea-VEAacid 2).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Abdominal perisymphathetic organs;  
RA Predel R.;  
RL Submitted (JUL-2000) to Swiss-Prot.  
CC -!- FUNCTION: Unknown.  
KW Neuropeptide.  
SQ SEQUENCE    15 AA;    1603 MW;    F353DC8B1F92B8BD CRC64;

Query Match                    43.8%;    Score 21;    DB 1;    Length 15;  
Best Local Similarity        80.0%;    Pred. No. 3.8e+02;  
Matches        4;    Conservative    1;    Mismatches    0;    Indels        0;    Gaps        0;

Qy            1 VESYV 5  
              |:| | |  
Db            9 VDSYV 13

RESULT 5

CXA1\_CONAL

ID CXA1\_CONAL            STANDARD;            PRT;        16 AA.  
AC P56639;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Alpha-conotoxin AuIA.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99003392; PubMed=9786965;  
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
RA Olivera B.M., McIntosh J.M.;  
RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic

RT acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide blocks mammalian nicotinic  
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; A59045; A59045.  
 DR HSSP; P50984; 1PEN.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 8  
 FT DISULFID 3 16  
 FT MOD\_RES 16 16 AMIDATION.  
 SQ SEQUENCE 16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;

Query Match 43.8%; Score 21; DB 1; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8  
 ||||  
 Db 4 SYPPCF 9

# RESULT 6

CXA3\_CONAL  
 ID CXA3\_CONAL STANDARD; PRT; 16 AA.  
 AC P56641;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin AuIC.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RA Olivera B.M., McIntosh J.M.;  
 RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic  
 RT acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide blocks mammalian nicotinic  
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; C59045; C59045.  
 DR HSSP; P50984; 1PEN.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 8  
 FT DISULFID 3 16  
 FT MOD\_RES 16 16 AMIDATION.  
 SQ SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;

Query Match 43.8%; Score 21; DB 1; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYVPLF 8  
 ||||  
 Db 4 SYPPCF 9

#### RESULT 7

##### PH3\_PERAM

ID PH3\_PERAM STANDARD; PRT; 17 AA.  
 AC P82696;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Peptide hormone 3 (Pea-VEAacid 1).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Abdominal perisymphathetic organs;  
 RX MEDLINE=20140865; PubMed=10676456;  
 RA Predel R., Eckert M., Holman G.M.;  
 RT "The unique neuropeptide pattern in abdominal perisymphathetic organs  
 RT of insects."  
 RL Ann. N.Y. Acad. Sci. 897:282-290(1999).  
 CC -!- FUNCTION: Unknown.  
 CC -!- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.  
 KW Neuropeptide.  
 SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F86E8EB CRC64;

Query Match 43.8%; Score 21; DB 1; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESYV 5  
 |:|||  
 Db 11 VDSYV 15

#### RESULT 8

## RF1\_CONSP

ID RF1\_CONSP STANDARD; PRT; 12 AA.  
AC P58805;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Conorfamide-Srl.  
OS Conus spurius (Alphabet cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=192919;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=21605839; PubMed=11738233;  
RA Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,  
RA Olivera B.M., Heimer de la Coteria E.P.;  
RT "Conorfamide, a Conus venom peptide belonging to the RFamide family of  
RT neuropeptides.";  
RL Toxicon 40:401-407(2002).  
CC -!- FUNCTION: Causes hyperactivity in mice.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
KW Neurotoxin; Toxin; Amidation.  
FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1456 MW; 2510671E49D772D3 CRC64;

Query Match 41.7%; Score 20; DB 1; Length 12;  
Best Local Similarity 60.0%; Pred. No. 4.7e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPLF 8  
:|:|  
Db 5 WVPVF 9

## RESULT 9

## SAL1\_ONCMY

ID SAL1\_ONCMY STANDARD; PRT; 15 AA.  
AC P81369;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Salmocidin 1 (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Serum;  
RA Henry M.A., Siegert K.J., Davidson I., Dunbar B., Mordue W.,

RA Secombes C.J.;  
 RT "Isolation and N-terminal sequencing of an antibacterial peptide in  
 RT rainbow trout, *Oncorhynchus mykiss*.";  
 RL Submitted (MAY-1998) to Swiss-Prot.  
 CC -!- FUNCTION: Antibacterial peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Plasma serum.  
 KW Antibiotic.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1586 MW; 3AF4AD95AFAB26D0 CRC64;

Query Match 41.7%; Score 20; DB 1; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 6e+02;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YVPLFP 9  
 | : | |  
 Db 10 YLPAXP 15

#### RESULT 10

##### TY13\_PHYRO

ID TY13\_PHYRO STANDARD; PRT; 13 AA.  
 AC P04096;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin-13.  
 OS Phyllomedusa rohdei (Rohde's leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Phyllomedusinae; Phyllomedusa.  
 OX NCBI\_TaxID=8394;  
 RN [1]  
 RP SEQUENCE.  
 RA Montecucchi P.C., Gozzini L., Erspamer V.;  
 RT "Primary structure determination of a tryptophan-containing  
 RT tridecapeptide from *Phyllomedusa rohdei*.";  
 RL Int. J. Pept. Protein Res. 27:175-182(1986).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 DR PIR; A05174; A05174.  
 KW Amphibian defense peptide; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 39.6%; Score 19; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 8.2e+02;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 | : : |  
 Db 9 PIYP 12

#### RESULT 11

##### ECDC\_LYMDI

ID ECDC\_LYMDI STANDARD; PRT; 14 AA.  
AC P80940;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Testis ecdysiotropin peptide C (TE).  
OS Lymantria dispar (Gypsy moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Lymantriidae; Lymantria.  
OX NCBI\_TaxID=13123;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=97387807; PubMed=9243792;  
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
RA Bell R.A.;  
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
RT gonadotropin isolated from brains of Lymantria dispar pupae."  
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).  
CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of  
CC larvae and pupae.  
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 39.6%; Score 19; DB 1; Length 14;  
Best Local Similarity 60.0%; Pred. No. 8.8e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVPL 7  
:| ||  
Db 6 AYTPL 10

# RESULT 12 COXJ\_THUOB

ID COXJ\_THUOB STANDARD; PRT; 15 AA.  
AC P80979;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIIa (EC 1.9.3.1) (Fragment).  
OS Thunnus obesus (Bigeye tuna).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
OX NCBI\_TaxID=8241;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart, and Liver;  
RX MEDLINE=97454291; PubMed=9310366;  
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
RA Kadenbach B.;  
RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
RT liver."  
RL Eur. J. Biochem. 248:99-103(1997).  
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide

CC chains of cytochrome c oxidase, the terminal oxidase in  
 CC mitochondrial electron transport.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIa family.  
 DR PIR; S77988; S77988.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT MOD\_RES 1 1 BLOCKED.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1769 MW; C111B99419E69A1E CRC64;

Query Match 39.6%; Score 19; DB 1; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 9.5e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6  
 :|||  
 Db 2 NYVP 5

# RESULT 13

## UPA1\_HUMAN

ID UPA1\_HUMAN STANDARD; PRT; 8 AA.  
 AC P30087;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.9, its MW is: 65 kDa.  
 DR SWISS-2DPAGE; P30087; HUMAN.  
 FT NON\_TER 1 1  
 FT UNSURE 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 37.5%; Score 18; DB 1; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVP 6  
 ||||  
 Db 3 ESNVP 7



# RESULT 14

PPK6\_PERAM

ID PPK6\_PERAM STANDARD; PRT; 14 AA.  
AC P82693;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-6 (Pea-PK-6) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.  
RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: Shows a weakly myoactive action.  
CC -!- TISSUE SPECIFICITY: Corpora alata and to a lesser extent in  
CC abdominal perisymphathetic organs.  
CC -!- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the pyrokinin family.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Amidation; Pyrokinin.  
FT MOD\_RES 14 14 AMIDATION.  
SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESYVP 6  
|| ||  
Db 2 ESEVP 6

# RESULT 15

ECDA\_LYMDI

ID ECDA\_LYMDI STANDARD; PRT; 15 AA.  
AC P80938;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Testis ecdysiotropin peptide A (TE).  
OS Lymantria dispar (Gypsy moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Lymantriidae; Lymantria.  
OX NCBI\_TaxID=13123;  
RN [1]

RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=97387807; PubMed=9243792;  
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
 RA Bell R.A.;  
 RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
 RT gonadotropin isolated from brains of Lymantria dispar pupae.";  
 RL Arch. Insect Biochem. Physiol. 36:37-50(1997).  
 CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes  
 CC of larvae and pupae.  
 SQ SEQUENCE 15 AA; 1712 MW; 12E8D8246B74EE26 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESYVPL 7  
 : | ||  
 Db 6 DEYEPL 11

# RESULT 16

## LPF\_ECOLI

ID LPF\_ECOLI STANDARD; PRT; 15 AA.  
 AC P03057;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phe leader peptide (Attenuator peptide).  
 GN PHEL OR PHEAE OR B2598 OR SF2658 OR S4807.  
 OS Escherichia coli, and  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562, 623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli;  
 RX MEDLINE=79033820; PubMed=360214;  
 RA Zurawski G., Brown K., Killingly D., Yanofsky C.;  
 RT "Nucleotide sequence of the leader region of the phenylalanine operon  
 RT of Escherichia coli.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli;  
 RX MEDLINE=91072346; PubMed=2254312;  
 RA Gavini N., Davidson B.E.;  
 RT "pheAo mutants of Escherichia coli have a defective pheA attenuator.";  
 RL J. Biol. Chem. 265:21532-21535(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;  
 RX MEDLINE=22272406; PubMed=12384590;  
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,  
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
 RA Yu J.;  
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity  
 RT through comparison with genomes of Escherichia coli K12 and O157.";  
 RL Nucleic Acids Res. 30:4432-4441(2002).

RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;  
 RX MEDLINE=22590274; PubMed=12704152;  
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,  
 RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,  
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,  
 RA Schwartz D.C., Blattner F.R.;  
 RT "Complete genome sequence and comparative genomics of Shigella  
 RT flexneri serotype 2a strain 2457T.";  
 RL Infect. Immun. 71:2775-2786(2003).  
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS  
 CC OF PHENYLALANINE.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----

DR EMBL; V00314; CAA23600.1; -.  
 DR EMBL; M10431; AAA24329.1; -.  
 DR EMBL; M58024; AAA62783.1; -.  
 DR EMBL; AE000346; AAC75647.1; -.  
 DR EMBL; AE015281; AAN44154.1; -.  
 DR EMBL; AE016987; AAP17979.1; -.  
 DR PIR; A03593; LFECF.  
 DR EcoGene; EG11271; pheL.  
 KW Leader peptide; Complete proteome.  
 SQ SEQUENCE 15 AA; 1924 MW; CFE14AE3BFF935E0 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YVPLF 8  
 ::| |  
 Db 3 HIPFF 7

# RESULT 17

UC17\_MAIZE

ID UC17\_MAIZE STANDARD; PRT; 15 AA.  
AC P80623;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 32)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 5.5, its MW is: 42.7 kDa.  
DR Maize-2DPAGE; P80623; COLEOPTILE.  
DR MaizeDB; 123949; -.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1554 MW; COAFFFF15FFECEEC8 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLF 8

||:|

Db 4 VPVF 7

# RESULT 18

UC30\_MAIZE

ID UC30\_MAIZE STANDARD; PRT; 15 AA.  
AC P80636;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 662)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program."  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.9, its MW is: 32.3 kDa.  
 DR Maize-2DPAGE; P80636; COLEOPTILE.  
 DR MaizeDB; 123961; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1545 MW; 3485190F4EF38018 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 |||  
 Db 5 PLLP 8

# RESULT 19

RM35\_YEAST

ID RM35\_YEAST STANDARD; PRT; 17 AA.  
 AC P36530;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Mitochondrial 60S ribosomal protein L35 (YmL35) (Fragment).  
 GN MRPL35.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91285106; PubMed=2060626;  
 RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,  
 RA Kitakawa M.;  
 RT "Extended N-terminal sequencing of proteins of the large ribosomal  
 RT subunit from yeast mitochondria."  
 RL FEBS Lett. 284:51-56(1991).  
 DR PIR; S17274; S17274.  
 DR GermOnline; 140814; -.  
 DR SGD; S0002730; MRPL35.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1826 MW; 6CE89CB415483EE8 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
 |::|  
 Db 12 PVYP 15

# RESULT 20

FIBB\_ANAPL

ID FIBB\_ANAPL STANDARD; PRT; 18 AA.  
AC P12802;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Anas platyrhynchos (Domestic duck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
OX NCBI\_TaxID=8839;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85168193; PubMed=3983613;  
RA Min Y., Ping Z., Yaoshi Z.;  
RT "Purification and primary structures of duck fibrinopeptides A and  
RT B.";  
RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).  
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that  
CC polymerize into fibrin and acting as a cofactor in platelet  
CC aggregation.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,  
CC which cleaves fibrinopeptides A and B from alpha and beta chains,  
CC and thus exposes the N-terminal polymerization sites responsible  
CC for the formation of the soft clot.  
DR PIR; JP0102; JP0102.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma; Sulfation; Pyrrolidone carboxylic acid.  
FT PEPTIDE 1 18 FIBRINOPEPTIDE B.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 6 6 SULFATION.  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 2028 MW; B0F15E7768F8A1F9 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 18;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESYVP 6  
|| ||  
Db 11 ESTVP 15

# RESULT 21

UPA7\_HUMAN

ID UPA7\_HUMAN STANDARD; PRT; 9 AA.  
AC P30093;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.05, its MW is: 37 kDa.  
 DR SWISS-2DPAGE; P30093; HUMAN.  
 FT NON\_TER 1 1  
 FT UNSURE 5 5  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match 35.4%; Score 17; DB 1; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.4e+05;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 SYVPLFP 9  
 | | | |  
 Db 1 SLVPEXP 7

# RESULT 22

## TM2A\_METMA

ID TM2A\_METMA STANDARD; PRT; 12 AA.  
 AC P80652;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
 DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M  
 DE methyltransferase 28 kDa subunit) (Fragment).  
 OS Methanosarcina mazei (Methanosarcina frisia).  
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=96370840; PubMed=8774736;  
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:  
 RT coenzyme M methyltransferase from Methanosarcina mazei Gol  
 RT reconstituted in ether lipid liposomes.";  
 RL Eur. J. Biochem. 239:857-864(1996).  
 CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
 CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
 CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
 CC TETRAHYDROMETHANOPTERIN.

CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
 CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
 CC (methylthio)ethanesulfonate.  
 CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 35.4%; Score 17; DB 1; Length 12;  
 Best Local Similarity 37.5%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9  
 | |:  
 Db 2 EKLEPVLP 9

# RESULT 23

## APID\_BOMPA

ID APID\_BOMPA STANDARD; PRT; 17 AA.  
 AC P81464;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Apidaecin.  
 OS Bombus pascuorum (Brown bumble bee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Apidae; Bombus.  
 OX NCBI\_TaxID=65598;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=97362903; PubMed=9219367;  
 RA Rees J.A., Moniatte M., Bulet P.;  
 RT "Novel antibacterial peptides isolated from a European bumblebee,  
 RT Bombus pascuorum (Hymenoptera, Apoidea).";  
 RL Insect Biochem. Mol. Biol. 27:413-422(1997).  
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
 CC bacteria.  
 CC -!- INDUCTION: By bacterial infection.  
 DR InterPro; IPR004828; Apidaecin.  
 DR Pfam; PF00807; Apidaecin; 1.  
 KW Insect immunity; Antibiotic; Hemolymph.  
 SQ SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match 35.4%; Score 17; DB 1; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
 |:  
 Db 6 YIP 8

# RESULT 24



LPK2\_LOCMI

ID LPK2\_LOCMI STANDARD; PRT; 10 AA.  
 AC P41488;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=94094539; PubMed=7903606;  
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustapyrokinin II from  
 RT Locusta migratoria, another member of the FXPRL-amide peptide  
 RT family.";  
 RL Comp. Biochem. Physiol. 106C:103-109(1993).  
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 CC activity).  
 CC -!- SIMILARITY: Belongs to the pyrokinin family.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VPLF 8  
 |||  
 Db 3 VPTF 6

RESULT 25

TKNB\_ONCMY

ID TKNB\_ONCMY STANDARD; PRT; 10 AA.  
 AC P28500;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neurokinin A (Substance K) (Neuromedin L).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and  
 OS Gadus morhua (Atlantic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022, 8049;  
 RN [1]  
 RP SEQUENCE.

RC SPECIES=O.mykiss, and G.morhua;  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23186; S23186.  
 DR PIR; S23307; S23307.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 10 AA; 1145 MW; 136B4062C9D5B440 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPL 7  
 : | : | |  
 Db 3 INSFVGL 9

#### RESULT 26

##### TKND\_RANCA

ID TKND\_RANCA STANDARD; PRT; 11 AA.  
 AC P22691;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatachykinin D (RTK D).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Intestine;  
 RX MEDLINE=91254337; PubMed=2043143;  
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
 RT brain and intestine.";  
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=94023216; PubMed=8210506;  
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and

RT intestine.";  
 RL Regul. Pept. 46:81-88(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D61033; D61033.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; FALSE\_NEG.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPL 7  
 | |:  
 Db 8 YAPM 11

#### RESULT 27

##### GRAR\_RANRU

ID GRAR\_RANRU STANDARD; PRT; 12 AA.  
 AC P40754;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Granuliberin-R.  
 OS Rana rugosa (Wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8410;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=78062810; PubMed=589733;  
 RA Nakajima T., Yasuhara T.;  
 RT "A new mast cell degranulating peptide, granuliberin-R, in the frog  
 RT (Rana rugosa) skin."  
 RL Chem. Pharm. Bull. 25:2464-2465(1977).  
 RN [2]  
 RP SYNTHESIS.  
 RX MEDLINE=78189201; PubMed=657408;  
 RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,  
 RA Koyama K., Yajima H.;  
 RT "Synthesis of the dodecapeptide amide corresponding to the entire  
 RT amino acid sequence of granuliberin-R, a new frog skin peptide from  
 RT Rana rugosa."  
 RL Chem. Pharm. Bull. 26:1222-1230(1978).  
 CC -!- FUNCTION: Mast cell degranulating peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Mast cell degranulation; Amidation.

FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 12;  
Best Local Similarity 20.0%; Pred. No. 2.9e+03;  
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPLF 8  
::|::  
Db 3 FLPIY 7

#### RESULT 28

##### ADFB\_TENMO

ID ADFB\_TENMO STANDARD; PRT; 13 AA.  
AC P83109;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Antidiuretic factor B (ADfb).  
OS Tenebrio molitor (Yellow mealworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Tenebrionidae; Tenebrio.  
OX NCBI\_TaxID=7067;  
RN [1]  
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND  
RP SYNTHESIS.  
RC TISSUE=Head;  
RX MEDLINE=22465067; PubMed=12576082;  
RA Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,  
RA Hull J.J., Schooley D.A.;  
RT "Isolation, identification and localization of a second beetle  
RT antidiuretic peptide."  
RL Peptides 24:27-34(2003).  
CC -!- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses  
CC cGMP as second messenger. May function as an antidiuretic  
CC hormone.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two  
CC pairs of bilaterally symmetrical cells in the protocerebrum.  
CC -!- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.  
KW Neuropeptide; Hormone.  
SQ SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;

Query Match 33.3%; Score 16; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYVP 6  
|||  
Db 5 SYKP 8

#### RESULT 29

##### YPE2\_LACLC

ID YPE2\_LACLC STANDARD; PRT; 13 AA.

AC P42021;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein in PEPT 5'region (ORF2) (Fragment).  
 OS *Lactococcus lactis* (subsp. *cremoris*) (*Streptococcus cremoris*).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; *Lactococcus*.  
 OX NCBI\_TaxID=1359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94245610; PubMed=8188586;  
 RA Mierau I., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,  
 RA Konings W.N., Venema G., Kok J.;  
 RT "Tripeptidase gene (pepT) of *Lactococcus lactis*: molecular cloning  
 RT and nucleotide sequencing of pepT and construction of a chromosomal  
 RT deletion mutant.";  
 RL J. Bacteriol. 176:2854-2861(1994).

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 CC -----

DR EMBL; L27596; AAA20625.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 13;  
 Best Local Similarity 28.6%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VESYVPL 7  
 :| :: |  
 Db 4 IEPFISL 10

# RESULT 30

HP29\_SARPE

ID HP29\_SARPE STANDARD; PRT; 16 AA.

AC P29184;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 29 kDa hemocyte proteinase (EC 3.4.22.-) (Fragment).

OS *Sarcophaga peregrina* (Flesh fly) (*Boettcherisca peregrina*).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

OC Sarcophagidae; Sarcophaga.

OX NCBI\_TaxID=7386;

RN [1]

RP SEQUENCE.

RC TISSUE=Pupal hemocytes;

RX MEDLINE=92174954; PubMed=1541301;

RA Kurata S., Saito H., Natori S.;  
 RT "Purification of a 29-kDa hemocyte proteinase of *Sarcophaga*  
 RT *peregrina*.";  
 RL Eur. J. Biochem. 204:911-914(1992).  
 CC -!- FUNCTION: Involved in the dissociation of the larval fat body on  
 CC metamorphosis.  
 CC -!- SIMILARITY: Belongs to peptidase family C1.  
 DR PIR; S21184; S21184.  
 DR InterPro; IPR000169; SHprot\_acsite.  
 DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE; PS00639; THIOI\_PROTEASE\_HIS; PARTIAL.  
 DR PROSITE; PS00640; THIOI\_PROTEASE\_ASN; PARTIAL.  
 KW Hydrolase; Thiol protease.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1815 MW; F70617AEB1E57351 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 16;  
 Best Local Similarity 60.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESYVP 6  
 :| ||  
 Db 1 DSXVP 5

# RESULT 31

## VPR\_HV1S3

ID VPR\_HV1S3 STANDARD; PRT; 16 AA.  
 AC P19555;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE VPR protein (R ORF protein) (Fragment).  
 GN VPR.  
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90317906; PubMed=2370688;  
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
 RT "Human immunodeficiency virus type 1 cellular host range,  
 RT replication, and cytopathicity are linked to the envelope region of  
 RT the viral genome.";  
 RL J. Virol. 64:4016-4020(1990).

-----  
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 CC -----

DR EMBL; M38427; AAA45066.1; -.  
 DR HIV; M38427; VPR\$SF33.  
 KW AIDS.

FT NON\_TER 1 1  
SQ SEQUENCE 16 AA; 1786 MW; 0C28AC9630029A56 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 4e+03;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVP 6  
:::|  
Db 11 QNWVP 15

RESULT 32

AHD2\_TETPY

ID AHD2\_TETPY STANDARD; PRT; 18 AA.  
AC P35430;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE 20-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) (20-alpha-HSD)  
DE (Fragment).  
OS Tetrahymena pyriformis.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
OC Tetrahymenina; Tetrahymena.  
OX NCBI\_TaxID=5908;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=W;  
RX MEDLINE=94107273; PubMed=8280099;  
RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;  
RT "Purification and characterization of a novel dimeric 20 alpha-  
RT hydroxysteroid dehydrogenase from Tetrahymena pyriformis.";  
RL Biochem. J. 297:195-200(1994).  
CC -!- FUNCTION: Specific for the oxidation of the 20-alpha hydroxy  
CC group of 17-alpha-hydroxyprogesterone and 17-alpha-  
CC hydroxypregnenolone.  
CC -!- CATALYTIC ACTIVITY: 17-alpha,20-alpha-dihydroxypregn-4-en-3-one +  
CC NAD(P)(+) = 17-alpha-hydroxyprogesterone + NAD(P)H.  
CC -!- SUBUNIT: Homodimer.  
DR PIR; S40502; S40502.  
KW Oxidoreductase; NADP.  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;

Query Match 32.3%; Score 15.5; DB 1; Length 18;  
Best Local Similarity 50.0%; Pred. No. 5.6e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 5 VPL-----FP 9  
||| ||  
Db 5 VPLNDGTNFP 14

RESULT 33

ALL6\_CYDPO

ID ALL6\_CYDPO STANDARD; PRT; 8 AA.  
AC P82157;

DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 6.  
 OS *Cydia pomonella* (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; *Cydia*.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
  
 Query Match 31.2%; Score 15; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 5 VPLF 8  
 :||:  
 Db 1 LPLY 4

RESULT 34  
 PPK3\_PERAM  
 ID PPK3\_PERAM STANDARD; PRT; 8 AA.  
 AC P82618;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).  
 OS *Periplaneta americana* (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; *Periplaneta*.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Retrocerebral complex;  
 RX MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
 RT "Differential distribution of pyrokinin-isoforms in cerebral and  
 RT abdominal neurohemal organs of the American cockroach."  
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of



RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 CC activity).  
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.  
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
 CC -!- SIMILARITY: Belongs to the pyrokinin family.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 VPLFP 9  
 || |  
 Db 2 VPFRP 6

# RESULT 35

## LMT3\_LOCFMI

ID LMT3\_LOCFMI STANDARD; PRT; 9 AA.  
 AC P41489;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Locustamyotropin 3 (LOM-MT-3).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustamyotropin III and  
 RT IV, two additional neuropeptides of Locusta migratoria: members of the  
 RT locustamyotropin peptide family."  
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
 CC -!- FUNCTION: Potent mediator of visceral muscle contractile activity  
 CC (myotropic activity).  
 CC -!- SIMILARITY: Belongs to the pyrokinin family.  
 DR PIR; A61620; A61620.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESYVP 6

Db                   : :||  
                    3 QPFVP 7

RESULT 36

RT02\_BOVIN  
ID RT02\_BOVIN       STANDARD;       PRT;     10 AA.  
AC P82923;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).  
GN MRPS2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=21276436; PubMed=11279123;  
RA Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;  
RT "The small subunit of the mammalian mitochondrial ribosome:  
RT identification of the full complement of ribosomal proteins present."  
RL J. Biol. Chem. 276:19363-19374(2001).  
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
CC       (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.  
DR InterPro; IPR001865; Ribosomal\_S2.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.  
KW Ribosomal protein; Mitochondrion.  
FT NON\_TER       1       1  
FT NON\_TER       10      10  
SQ SEQUENCE     10 AA;   1246 MW;   6A7A6679C04B476B CRC64;

Query Match                   31.2%;   Score 15;   DB 1;   Length 10;  
Best Local Similarity       40.0%;   Pred. No. 3.8e+03;  
Matches       2;   Conservative       2;   Mismatches     1;   Indels       0;   Gaps       0;

Qy               1 VESYV 5  
                 :| |:  
Db               2 MEPYI 6

RESULT 37

TKNB\_CHICK  
ID TKNB\_CHICK       STANDARD;       PRT;     10 AA.  
AC P19851;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Neurokinin A (Substance K) (Neuromedin L).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=88204263; PubMed=2452461;  
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";  
 RL Regul. Pept. 20:171-180(1988).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; JN0024; JN0024.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1134 MW; 8A6B4062C9D5BAB1 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESYVPL 7  
 :|:| |  
 Db 4 DSFVGL 9

# RESULT 38

## TKNB\_RANRI

ID TKNB\_RANRI STANDARD; PRT; 10 AA.  
 AC P29135;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neurokinin A.  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=93075037; PubMed=1332683;  
 RA Wang Y., Badgery-Parker T., Lovas S., Chartrel N., Vaudry H.,  
 RA Burcher E., Conlon J.M.;  
 RT "Primary structure and receptor-binding properties of a neurokinin A-  
 RT related peptide from frog gut.";  
 RL Biochem. J. 287:827-832(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S27178; S27178.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1160 MW; 526B407059D5BAA7 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 10;  
 Best Local Similarity 28.6%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VESYVPL 7  
 ::|::|  
 Db 3 LDSFIGL 9

# RESULT 39

## UPA8\_HUMAN

ID UPA8\_HUMAN STANDARD; PRT; 10 AA.  
 AC P30094;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 7.2, its MW is: 16 kDa.  
 DR SWISS-2DPAGE; P30094; HUMAN.  
 FT NON\_TER 1 1  
 FT VARIANT 4 4 S -> H.  
 FT /FTId=VAR\_000003.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 3.8e+03;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
 | | | |  
 Db 2 VGSKXPAVP 10

RESULT 40

NUDM\_CANFA

ID NUDM\_CANFA STANDARD; PRT; 12 AA.  
 AC P54713;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Complex I-42KD) (CI-42KD) (Fragment).  
 GN NDUFA10.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: Transfer of electrons from NADH to the respiratory  
 CC chain. The immediate electron acceptor for the enzyme is believed  
 CC to be ubiquinone.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -!- COFACTOR: Binds 1 FAD per subunit.  
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
 CC This a component of the hydrophobic protein fraction.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 DR HSC-2DPAGE; P54713; DOG.  
 KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YVPL 7  
 | ||  
 Db 3 YGPL 6

RESULT 41

CRBL\_VESCR

ID CRBL\_VESCR STANDARD; PRT; 13 AA.  
 AC P01518;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Crabrolin.  
 OS Vespa crabro (European hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7445;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=84289390; PubMed=6206053;  
 RA Argiolas A., Pisano J.J.;  
 RT "Isolation and characterization of two new peptides, mastoparan C and  
 RT crabrolin, from the venom of the European hornet, *Vespa crabro*.";   
 RL J. Biol. Chem. 259:10106-10111(1984).  
 RN [2]  
 RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.  
 RX MEDLINE=97419326; PubMed=9273892;  
 RA Krishnakumari V., Nagaraj R.;  
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue  
 RT peptide from the venom of the European hornet, *Vespa crabro*, and its  
 RT analogs.";   
 RL J. Pept. Res. 50:88-93(1997).  
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils. Has antimicrobial and hemolytic activity.  
 DR PIR; A01781; JZVHPL.  
 KW Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1497 MW; 515EF8FCEA8D2407 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 5e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
 :|||  
 Db 1 FLPL 4

#### RESULT 42

##### HPB9\_RANES

ID HPB9\_RANES STANDARD; PRT; 13 AA.  
 AC P32416;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hemolytic protein B9 (Fragment).  
 OS Rana esculenta (Edible frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90198965; PubMed=2317508;  
 RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,  
 RA Barra D., Bossa F.;  
 RT "Purification and characterization of bioactive peptides from skin  
 RT extracts of *Rana esculenta*.";   
 RL Biochim. Biophys. Acta 1033:318-323(1990).  
 CC -!- FUNCTION: Shows hemolytic activity.  
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.  
DR PIR; S09019; S09019.  
KW Amphibian defense peptide; Amidation; Hemolysis.  
FT MOD\_RES 13 13 AMIDATION.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 31.2%; Score 15; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 5e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
::||  
Db 1 FLPL 4

RESULT 43

PSAJ\_PEA

ID PSAJ\_PEA STANDARD; PRT; 13 AA.  
AC P17229;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem I reaction center subunit IX (PSI-J) (Fragment).  
GN PSAJ.  
OS Pisum sativum (Garden pea).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90242987; PubMed=2185953;  
RA Ikeuchi M., Hirano A., Hiyama T., Inoue Y.;  
RT "Polypeptide composition of higher plant photosystem I complex.  
RT Identification of psaI, psaJ and psaK gene products.";  
RL FEBS Lett. 263:274-278(1990).  
CC -!- FUNCTION: May help in the organization of the psaE and psaF  
CC subunits.  
CC -!- SIMILARITY: Belongs to the psaJ family.  
DR PIR; S09733; S09733.  
DR HAMAP; MF\_00522; -; 1.  
KW Chloroplast; Photosystem I; Photosynthesis; Transmembrane.  
FT TRANSMEM 7 >13 POTENTIAL.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1516 MW; 9E2E45D11FDE3B41 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 13;  
Best Local Similarity 22.2%; Pred. No. 5e+03;  
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VESYVPLFP 9  
::|: : |  
Db 4 LKTYLXVAP 12

RESULT 44

TEMA\_RANTE

ID TEMA\_RANTE STANDARD; PRT; 13 AA.  
 AC P56917;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Temporin A.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana  
 RT temporaria.";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 5e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
 ::||  
 Db 1 FLPL 4

RESULT 45

TEMF\_RANTE

ID TEMF\_RANTE STANDARD; PRT; 13 AA.  
 AC P56921;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Temporin F.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;



RT "Temporins, antimicrobial peptides from the European red frog *Rana*  
 RT *temporaria*";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-negative and  
 CC Gram-positive bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 5e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
 ::||  
 Db 1 FLPL 4

#### RESULT 46

##### CRBL\_VESOR

ID CRBL\_VESOR STANDARD; PRT; 14 AA.  
 AC P17236;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Histamine releasing peptide II (HR-II).  
 OS *Vespa orientalis* (Oriental hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; *Vespa*.  
 OX NCBI\_TaxID=7447;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,  
 RA Rozynov B.V., Gushchin I.S.;  
 RT "Structure and properties of histamine releasing peptides from the  
 RT venom of *Vespa orientalis* hornet."  
 RL Bioorg. Khim. 7:1467-1477(1981).  
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils.  
 DR PIR; JN0390; JN0390.  
 KW Mast cell degranulation; Chemotaxis; Amidation.  
 FT MOD\_RES 14 14 AMIDATION.  
 SQ SEQUENCE 14 AA; 1524 MW; 22015B4A6CEDFD38 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
 ::||  
 Db 1 FLPL 4

# RESULT 47

LPK1\_LOCMI

ID LPK1\_LOCMI STANDARD; PRT; 16 AA.  
AC P20404;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Locustapyrokinin 1 (LOM-PK-1).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=91224474; PubMed=2026322;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a  
RT myotropic peptide of Locusta migratoria."  
RL Gen. Comp. Endocrinol. 81:97-104(1991).  
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
CC activity).  
CC -!- SIMILARITY: Belongs to the pyrokinin family.  
DR PIR; A49761; A49761.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 16 16 AMIDATION.  
SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 6.2e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESYVP 6  
: :||  
Db 10 QPFVP 14

# RESULT 48

MLB\_SQUAC

ID MLB\_SQUAC STANDARD; PRT; 16 AA.  
AC P01207;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanotropin beta.  
OS Squalus acanthias (Spiny dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squalia; Squaloidei; Squalidae; Squalus.  
OX NCBI\_TaxID=7797;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75127390; PubMed=4375978;

RA Bennett H.P.J., Lowry P.J., McMartin C., Scott A.P.;  
 RT "Structural studies of alpha-melanocyte-stimulating hormone and a  
 RT novel beta-melanocyte-stimulating hormone from the neurointermediate  
 RT lobe of the pituitary of the dogfish *Squalus acanthias*.";  
 RL Biochem. J. 141:439-444(1974).  
 CC -!- SIMILARITY: Belongs to the POMC family.  
 DR PIR; A01471; MTDFBS.  
 KW Hormone.  
 SQ SEQUENCE 16 AA; 1939 MW; 993AF43C8A640A0E CRC64;

Query Match 31.2%; Score 15; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7  
 |||  
 Db 14 VPL 16

#### RESULT 49

ALL2\_CYDPO

ID ALL2\_CYDPO STANDARD; PRT; 18 AA.  
 AC P82153;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 2.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricodea; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 18 18 AMIDATION.  
 SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;

Query Match 31.2%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5  
 |||  
 Db 3 SYV 5

#### RESULT 50

CPAX\_BOVIN

ID CPAX\_BOVIN STANDARD; PRT; 18 AA.

AC P22779;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Cytochrome P450 2A (OLF2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91027757; PubMed=2121272;  
 RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;  
 RT "Identification and biochemical analysis of novel olfactory-specific  
 RT cytochrome P-450IIA and UDP-glucuronosyl transferase.";  
 RL Biochemistry 29:7433-7440(1990).  
 CC -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate  
 CC monooxygenases. In liver microsomes, this enzyme is involved in an  
 CC NADPH-dependent electron transport pathway. It oxidizes a variety  
 CC of structurally unrelated compounds, including steroids, fatty  
 CC acids, and xenobiotics.  
 CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -!- SIMILARITY: Belongs to the cytochrome P450 family.  
 DR PIR; A35704; A35704.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; PARTIAL.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Microsome; Endoplasmic reticulum; Olfaction.  
 FT NON\_TER 1 1  
 FT VARIANT 6 6 G -> D.  
 FT VARIANT 11 11 A -> E.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match 31.2%; Score 15; DB 1; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
 |:  
 Db 3 YLP 5

Search completed: July 4, 2004, 04:41:32  
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